3S

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification⁷: C12N

(21) International Application Number: PCT/US01/07771

(22) International Filing Date: 13 March 2001 (13.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/188,914	13 March 2000 (13.03.2000)	US
60/192,033	24 March 2000 (24.03.2000)	US
60/198,474	12 April 2000 (12.04.2000)	US
60/199,335	24 April 2000 (24.04.2000)	US
60/207,702	26 May 2000 (26.05.2000)	US
60/213,849	23 June 2000 (23.06.2000)	US
60/226,534	16 August 2000 (16.08.2000)	US
60/230,732	7 September 2000 (07.09.2000)	US
60/266,862	7 February 2001 (07.02.2001)	US

(71) Applicant: SENOMYX, INC. [US/US]; Suite 160, 11099 N. Torrey Pines Road, La Jolla, CA 92037 (US).

(72) Inventor: ZOZULYA, Sergey; 3950 Mahaila Avenue #B22, San Diego, CA 92122 (US).

(74) Agents: TESKIN, Robin, L. et al.; Pillsbury Winthrop LLP, 1100 New York Avenue, NW, Washington, DC 20005 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/68805 A2

(54) Title: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

(57) Abstract: Newly identified Olfactory G protein-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, G protein-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. Methods for representing olfactory perception of a particula odorant are also described, as are methods for generating novel molecules or combinations of molecules that elicit a predetermined odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed.

HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S.
5   Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY
RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No.
60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS
AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed
April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE
10   ENCODING THE SAME to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000,
"HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to
Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN
OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya;
U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY
15   RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No.
60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND
GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed
September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES
ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February
20   7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE
SAME", to Zozulya. All of these applications are herein incorporated by reference in
their entireties.

Field of the Invention

25   The invention relates to newly identified mammalian chemosensory G protein-
coupled receptors, particularly olfactory receptors, fragments thereof, classes of such
receptors, genes and cDNAs encoding said receptors, vectors including said receptors,
and cells that express said receptors. The invention also relates to methods of using
such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules
30   involved in olfactory perception. The invention therefore has application in the
selection and design of odorant compositions, as well as malodor blockers (olfactory
receptor antagonists), particularly perfumes and fragrance compositions and
components of deodorants and other malodor blocking compositions.

-1-

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis, carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

-2-

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains

5 approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25

10 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic

15 tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can

20 respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by

25 binding assays.

Some studies suggest that OR genes can be expressed in tissues other that the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor*

30 *Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthier, *Nature,* 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. *See, e.g.,* Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); *see also,* EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

-4-

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204. SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

NO. 224, SEQ. ID. NO. 226, SEQ. ID. NO. 228, SEQ. ID. NO. 230, SEQ. ID.
NO. 232, SEQ. ID. NO. 234, SEQ. ID. NO. 236, SEQ. ID. NO. 238, SEQ. ID
NO. 240, SEQ. ID. NO. 242, SEQ. ID. NO. 244, SEQ. ID. NO. 246, SEQ. ID. NO.
248, SEQ. ID. NO. 250, SEQ. ID. NO. 252, SEQ. ID. NO. 254, SEQ. ID. NO. 256,
5   SEQ. ID. NO. 258, SEQ. ID. NO. 260, SEQ. ID. NO. 262, SEQ. ID. NO. 264, SEQ.
ID. NO. 266, SEQ. ID. NO. 268, SEQ. ID. NO. 270, SEQ. ID. NO. 272, SEQ. ID.
NO. 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282,
SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID
NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300,
10 SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID
NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318,
SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID
NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336,
SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID
15 NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354,
SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID
NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370 ,SEQ ID NO: 372,
SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID
NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390,
20 SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID
NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408,
SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID
NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426,
SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID
25 NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444,
SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID
NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462,
SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID
NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480,
30 SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID
NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498,
SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID
NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

-7-

NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
5   NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
10   311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
15   SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
20   NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
25   439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
30   SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:
499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ
ID NO: 509 and SEQ ID NO: 511.

-8-

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100, or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5   It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ.

10   ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61,

15   SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID.

20   NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

25   NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID.

30   NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.
NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.
NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
5   SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
10   ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
15   NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
20   SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
25   ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
30   NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

-13-

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,

SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.

ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.

NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.

5   277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,

SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.

ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.

NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.

311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,

10   SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.

ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.

NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.

345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,

SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.

15   ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:

371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,

SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.

ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.

NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.

20   405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,

SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.

ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.

NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.

439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,

25   SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.

ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.

NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.

473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,

SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.

30   ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ

ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60,

80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and quantitative level , wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

-15-

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitutes a point or a volume in n-dimensional space, may constitutes a graph or a spectrum, and may constitutes a matrix of quantitative representations. Also, the

-16-

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5   Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences
10   AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

        Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins
15   described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

        Figure 3 illustrates the multiple sequence alignment derived for fifty novel
20   ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the
25   AOLF110 amino acid sequence.

        Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The
30   alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

-18-

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The

5   alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

10   The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al., Cell*, 95:917-26 (1998), and WO 0035274,

15   the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones

20   (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112,

25   AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088,

30   AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

-19-

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083,

5   AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959,

10   AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically

15   engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also

20   serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-inducted behaviors.

The invention also provides methods of screening for modulators, *e.g.*,

25   activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These

30   modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

-20-

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro, in*
5   *vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.,* Mistili *et al., Nature Biotech.,* 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by
10   measuring changes in Ca^{2+} levels.

  Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of
15   such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.
20   The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can
25   be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A^+ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

  A. **Identification and Characterization of Olfactory Receptors**

30   The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J *Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS,* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection *(see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.,* eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

-22-

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating

5   searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a

10   scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and

15   X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix *(see* Henikoff & Henikoff, *PNAS,* 89:10915 (1989))

20   alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-

25   called "tree" or "dendogram" showing the clustering relationships used to create the alignment *(see, e.g.,* Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, CABIOS 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of

30   5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

-23-

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using

5   PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g., version 7. 0 (Devereaux et al., Nuc. Acids Res. 12:387-395 (1984) encoded by the genes were

10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most

15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as

20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close

25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of

30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

-24-

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore,

5   these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B.   Definitions

10   As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

"OR" refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g.*, Roper, *supra*), or by the expression of

15   proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

"OR" nucleic acids encode a family of GPCRs with seven transmembrane regions that have "G protein-coupled receptor activity," *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second

20   messengers such as IP3, cAMP, cGMP, and Ca^{2+} via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g.*, Fong, *supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an "N-terminal domain;"

25   "extracellular domains;" "transmembrane domains" comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; "cytoplasmic domains," and a "C-terminal domain" (*see, e.g.*, Hoon *et al.*, *Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs

30   that identify hydrophobic and hydrophilic domains (*see, e.g.*, Stryer, *Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

-25-

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

"Extracellular domains" therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the "N terminal domain" that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The "N terminal domain" region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. "Transmembrane domain," which comprises the seven "transmembrane regions," refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

"Cytoplasmic domains" refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the "C terminal domain" and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. "C terminal domain" refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term "ligand-binding region" or "ligand-binding domain" refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the

5   determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP,

10   IP3, or intracellular Ca^{2+}), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly

15   under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents,

20   radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

25   "Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation,

30   inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

-27-

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

-28-

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5   As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or

10   compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processed known to those of skill in the

15   art.

          As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.,* specific degenerate oligonucleotide

20   primer pairs) for amplifying (*e.g.,* by polymerase chain reaction, PCR) naturally expressed (*e.g.,* genomic or mRNA) or recombinant (*e.g.,* cDNA) nucleic acids of the invention (*e.g.,* tastant-binding sequences of the invention) *in vivo* or *in vitro.*

          The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma

25   membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30   The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

-29-

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded

5   form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides.   The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); Antisense Strategies, *Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan

10   *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata; *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev, 6*:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly

15   encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated.   Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al., Nucleic*

20   *Acid Res.*, 19:5081 (1991); Ohtsuka *et al., J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al., Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid

25   polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into the amino terminus

30   of a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

-30-

functionally   equivalent   to   an   exemplary   translocation   domain   (5'-
MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any
mammal may be used, as can other translocation facilitating sequences. Thus, the
translocation domain is particularly efficient in translocating 7-transmembrane fusion

5   proteins to the plasma membrane, and a protein (e.g., an olfactory receptor
polypeptide) comprising an amino terminal translocating domain will be transported
to the plasma membrane more efficiently than without the domain. However, if the
N-terminal domain of the polypeptide is active in binding, the use of other
translocation domains may be preferred.

10   "Functional equivalency" means the domain's ability and efficiency in
translocating newly translated proteins to the plasma membrane as efficiently as
exemplary SEQ ID NO: 518 under similar conditions; relatively efficiencies an be
measured (in quantitative terms) and compared, as described herein. Domains falling
within the scope of the invention can be determined by routine screening for their

15   efficiency in translocating newly synthesized polypeptides to the plasma membrane in
a cell (mammalian, Xenopus, and the like) with the same efficiency as the twenty
amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The "translocation domain," "ligand-binding domain", and chimeric receptors
compositions described herein also include "analogs," or "conservative variants" and

20   "mimetics" ("peptidomimetics") with structures and activity that substantially
correspond to the exemplary sequences. Thus, the terms "conservative variant" or
"analog" or "mimetic" refer to a polypeptide which has a modified amino acid
sequence, such that the change(s) do not substantially alter the polypeptide's (the
conservative variant's) structure and/or activity, as defined herein. These include

25   conservatively modified variations of an amino acid sequence, i.e., amino acid
substitutions, additions or deletions of those residues that are not critical for protein
activity, or substitution of amino acids with residues having similar properties (e.g.,
acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the
substitutions of even critical amino acids does not substantially alter structure and/or

30   activity. Conservative substitution tables providing functionally similar amino acids
are well known in the art.

More particularly, "conservatively modified variants" applies to both amino
acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

-31-

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids

5   encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10   Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only

15   codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative

20   substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that

25   are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (see also, e.g., Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*

30   *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

-32-

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

5   The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, e.g., translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can

10   also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

       As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the

15   invention, i.e., that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues

20   which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or

25   coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., -C(=O)-CH$_2$- for -C(=O)-NH-), aminomethylene (CH$_2$-NH), ethylene, olefin

30   (CH=CH), ether (CH$_2$-O), thioether (CH$_2$-S), tetrazole (CN$_4$), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola, Chemistry and Biochemistry of Amino Acids, Peptides and Proteins, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

-33-

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

5   A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter
10   that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the
15   expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other
20   biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the
25   invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

30   The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

-35-

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60° C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60, or more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

An "anti-OR" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term "immunoassay" is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase "specifically (or selectively) binds" to an antibody or, "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

-37-

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or

5   polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive

10 with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g.,* Harlow & Lane, *Antibodies, A Laboratory Manual,* (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity). Typically a specific or selective reaction will be at least twice

15 background signal or noise and more typically more than 10 to 100 times background.

       The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

       The term "expression vector" refers to any recombinant expression system for

20 the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo,* constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e.,

25 drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

       By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic

30 cells such as E. toll, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo.*

-38-

C.   **Isolation and Expression of Olfactory Receptors**

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

-39-

See, e.g., Sambrook, ed., Molecular Cloning: a Laboratory manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); Current Protocols in Molecular Biology, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I,

5   Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.,* analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid

10   chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, *e.g.,* fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.,* SDS-

15   PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned

20   or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, *e.g.,* polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y.

25   (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (*see, e.g.,* Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (*see, e.g.,* Kwoh, *PNAS,* 86:1173 (1989)); and, self-sustained sequence replication (*see, e.g.,* Guatelli, *PNAS,* 87:1874 (1990)); Q Beta replicase amplification (*see, e.g.,*

30   Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (*see, e.g.,* Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (*e.g.,* NASBA, Cangene, Mississauga, Ontario); *see* also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

-40-

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of

5   vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp El sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that,

10   when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises

15   substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp El sequence in he primers of the invention generate an insert that, when ligated into the Pst I/Bsp El cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues

20   that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of

25   olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through

30   VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3') 3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as http://blocks.fhcrc.org/codehop.html, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g.*, Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

-42-

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial

5   nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g.*, Hoops, *Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the

10 shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g.*, Morales, *Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g.*, Hill, *PNAS,*

15 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

20 Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

(a)   5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)

25 (C/T)T-3' (SEQ ID NO: 525).

(b)   5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)
(C/T)T-3' (SEQ ID NO: 527)

30 (c)   5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)
(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)
(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be

35 generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using

-43-

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

5   Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,

10   *PNAS,* 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be

15   used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in

20   culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked

25   to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the

30   desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

-44-

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural

5   sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

        In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional

10   elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the

15   FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

        The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.,* Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.,* Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane

20   expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.,* Williams, *Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate

25   detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g.,* Kroll, *DNA Cell. Biol.* 12:441-53 (1993)).

30   Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

-45-

literature (*see, e.g.*, Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from

5   natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.*, episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer

10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.*, chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.*, chlorosulfuron or Basta) to permit selection of those cells

15 transformed with the desired DNA sequences (*see, e.g.*, Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

20   A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have

25 similar primary sequences and secondary and tertiary structures, structural domains (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that

30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); http://bioinfo.weizmann.ac.il/.

5   The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

          Libraries of olfactory receptor ligand-binding TM domain sequences can
10   include a various TM domains or variations thereof, as described above.   These sequences can be derived from any 7-transmembrane receptor.   Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel
15   *supra*), as described above.   Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

          The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
20   for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

          Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another
25   G protein receptor, preferably a member of the 7TM superfamily.   These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins.   In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the
30   remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known.   Thus, this knowledge of those skilled

-47-

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β-gal, glutamtate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, i.e., which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

-48-

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.*
However, bacterial or eukaryotic expression systems can be used.

5   Any of the well-known procedures for introducing foreign nucleotide
sequences into host cells may be used. These include the use of calcium phosphate
transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection,
plasma vectors, viral vectors and any of the other well known methods for introducing
cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a
host cell (*see, e.g.,* Sambrook *et al.*) It is only necessary that the particular genetic
engineering procedure used be capable of successfully introducing at lest one gene
10   into the host cell capable of expressing the olfactory receptor, fragment, or variant of
interest.

          After the expression vector is introduced into the cells, the transfected cells are
cultured under conditions favoring expression of the receptor, fragment, or variant of
interest, which is then recovered from the culture using standard techniques.
15   Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593,
which is incorporated by reference in a manner consistent with this disclosure.

D.   Immunological Detection of OR Polypeptides

          In addition to the detection of OR genes and gene expression using nucleic
acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to
20   identify olfactory receptor cells, and variants of OR family members. Immunoassays
can be used to qualitatively or quantitatively analyze the ORs. A general overview of
the applicable technology can be found in Harlow & Lane, Antibodies: A Laboratory
Manual (1988).

1.   Antibodies to OR family members

25   Methods of producing polyclonal and monoclonal antibodies that react
specifically with a OR family member are known to those of skill in the art (*see, e.g.,*
Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, supra; Goding,
Monoclonal Antibodies: Principles and Practice (2d ed. 1986); and Kohler &
Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation
30   by selection of antibodies from libraries of recombinant antibodies in phage or similar
vectors, as well as preparation of polyclonal and monoclonal antibodies by

-49-

immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275-81 (1989); Ward *et al.*, *Nature*, 341:544-46 (1989)).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see* Harlow & Lane, *supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see* Kohler & Milstein, *Eur. J. Immunol.*, 6:511-19 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

-50-

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5   Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other

10   organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a Kd of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

        Once OR family member specific antibodies are available, individual OR

15   proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20   **2.   Immunological binding assays**

        OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see* also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, *ed.* 1993);

25   *Basic and Clinical Immunology* (Stites & Terr, *eds.*, 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30   Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

-51-

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G

5   may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g.,* Kronval *et al., J. Immunol.,* 111:1401-1406 (1973); *Akerstrom et al., J. Immunol.,* 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10   A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution,

15   concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a.   Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either

20   competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a

25   labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.,* streptavidin, to

30   provide a detectable moiety.

b.   C mpetitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. **Cross-reactivity determinations**

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

-53-

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

5   The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding

10   of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15   Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

      Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using

20   other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d.   <u>Other assay formats</u>

25   Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that

30   specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

-54-

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see* Monroe *et al.*, *Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5   **e.   Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific

10   binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f.   Labels

15   The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such

20   methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS^{TM}) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ^{3}H, ^{125}I, ^{35}S, ^{14}C,

25   or ^{32}P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety

30   of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

-55-

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a

5   fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest

10   as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or

15   signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate

20   wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric

25   labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target

30   antibodies. I n this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

-56-

E.   Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

-57-

NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID.
NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID.
NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID.
NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID.
5   NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID.
NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID.
NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID.
NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID.
NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID.
10   NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID.
NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID.
NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID.
NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID.
NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO.
15   241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249,
SEQ. ID. NO. 251, SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ.
ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID.
NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO.
275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283,
20   SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ.
ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID.
NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO.
309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317,
SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ.
25   ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID.
NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO.
343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351,
SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ.
ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID.
30   NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO.
377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385,
SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ.
ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID.

-58-

NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO.
411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419,
SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ.
ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID.

5   NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO.
445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453,
SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ.
ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID.
NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO.

10 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487,
SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID
NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, or conservatively modified
variant thereof.

15   Alternatively, the OR protein of the assay can be derived from a eukaryote host
cell and can include an amino acid subsequence having at least about 30-40% amino
acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID.
NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ.
ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25,

20 SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID.
NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43,
SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID.
NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61,
SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID.

25 NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79,
SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID.
NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97,
SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID.
NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID.

30 NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID.
NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID.
NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID.
NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

-59-

NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID.

NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID.

NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID.

NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID.

NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID.

NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID.

NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID.

NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID.

NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.

NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,

SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.

ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.

NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.

277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,

SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.

ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.

NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.

311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,

SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.

ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.

NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.

345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,

SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.

ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:

371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,

SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.

ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.

NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.

405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,

SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.

ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.

5   ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

10 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain,

15 transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and

20 protein level, but also significant dissimilarly. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are

25 compared. However, while there exist differences, there are characteristic similarities, *e.g.* the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated,

30 expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1.   In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbence, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

-62-

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTPγS assay may be used. As described above, upon activation of a GPCR, the Gα subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTPγ^{35}S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTPγS are added to the assay, and binding of GTPγS to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTPγS can be utilized.

2.   Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

-63-

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand,

5   it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\text{II}} - Int_{\perp}}{Int_{\text{II}} + Int_{\perp}}$$

10   Where II is the intensity of the emission light parallel to the excitation light plane and $Int \perp$ is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000 ™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1

15   Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the

20   rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5° Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\,Re\,laxation\,Time = \frac{3\eta V}{RT}$$

25   The rotational relaxation time is small ($\approx$ 1 nanosecond) for small molecules (*e.g.* fluorescein) and large ($\approx$ 100 nanoseconds) for large molecules (*e.g.* immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules,

30   dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

-64-

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3.   Solid state and soluble high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (e.g., 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, e.g., via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (e.g., the olfactory transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

-65-

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals
5   1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody
10   and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,
15   immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;
20   peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,
25   polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about
30   5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

-66-

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example,

5   groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.,* Merrifield, *J. Am. Chem. Soc.,* 85:2149-54 (1963) (describing

10   solid phase synthesis of, *e.g.,* peptides); Geysen *et al., J. Immun. Meth.,* 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron,* 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al., Science,* 251:767-77 (1991); *Sheldon et al., Clinical Chemistry,* 39(4):718-19 (1993); and Kozal *et al., Nature Medicine,* 2(7):753759

15   (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4.   Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves

20   computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the

25   protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.,* ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding

30   nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

-67-

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID

NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID

NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID

NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

5   NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID

NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID

NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID

NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,

10   SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID

NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,

SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID

NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,

SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

15   NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,

SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID

NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,

SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,

20   SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID

NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID

25   NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,

SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,

SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

30   SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,

SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID

NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

-68-

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and
conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of
the protein, which encodes the structural information of the protein. At least 10
residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino
acids) are entered into the computer system from computer keyboards, computer
readable substrates that include, but are not limited to, electronic storage media (e.g.,
magnetic diskettes, tapes, cartridges, and chips), optical media (e.g., CD ROM),
information distributed by internet sites, and by RAM. The three-dimensional
structural model of the protein is then generated by the interaction of the amino acid
sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the
information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der

5   Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then

10   formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, e.g., cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the

15   computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of

20   compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25   Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used

30   to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

-70-

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified. Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5.   Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, e.g., $G\alpha15$, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, see, e.g., *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

-71-

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100.
Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (i.e., electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, e.g., the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (see, e.g., Ackerman et al., New Engl. J Med., 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (see, e.g., Vestergarrd-Bogind et al., J. Membrane Biol., 88:67-75 (1988); Gonzales & Tsien, Chem. Biol., 4:269277 (1997); Daniel et al., J. Pharmacol. Meth., 25:185-193 (1991); Holevinsky et al., J. Membrane Biology, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+}, IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

-72-

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed

5   in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as $G\alpha 15$ and $G\alpha 16$ can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,

10 increases in second messengers such as IP3, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in

15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3 can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in

20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are

25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents

30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-crated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

-73-

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

5   In a preferred embodiment, OR protein activity is measured by expressing a OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is $G\alpha15/G\alpha16$

10 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

15   In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein

20 incorporated by reference.

     In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and

25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the

30 presence of buffer control (which may or may not contain an agonist).

     In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

-74-

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.*, Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

6.   Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

-75-

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

5   Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable
10   responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinate bones facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate
15   bones and moved together up toward the top of the bone. *See also,* Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezeh, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*
20   *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal
25   nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS,* 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type
30   (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

-76-

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or 5 completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is 10 typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential 15 embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g.,* see Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 20 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or 25 rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F.   Modulators

30   The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to

5   screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (*e.g.*, in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka

10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, purfumes, fragrance compositions, deorderants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As

15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desireable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such

20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a

30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

-78-

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other

5   chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides

10   (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl

15   phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries

20   (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially
25   available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia,

30   MD; *etc.*).

G.   Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the

5   receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a

10   method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the

15   representation may constitutes a point or a volume in n-dimensional space, may constitutes a graph or a spectrum, and may constitutes a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

20   Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4,

25   for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of

30   said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

-80-

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or

5   combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10   In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of

15   molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of

20   molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

       In another embodiment of the invention, there is provided a method for

25   simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the

30   fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

-81-

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H.   Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.,* OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al., Biotechniques*, 4:230-50 (1986); Haase *et al., Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.,* eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and

5 reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

10   **EXAMPLES**

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human

15 olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

20 In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

25   EXAMPLES

AOLFR1 sequences:
MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIVAISLD
TYLHTPMYLFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVVIDNLLLGTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALTHTLLLIQLLFCNHNTLPHFFCDLAPLL
30 KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGKWKAFSTCGSHLTVVLLFY
GTTVGVYFFPSSTHPEDTDKIGAVLFTVVTPMINPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
35 CCATCACTGAATTCATTCTCCTGGGATTTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT
GATATTTCCTCCATTTCCAACTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

-83-

```
      AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTCGTCATT
      GACAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCCTCTGA
      ATTATACAATTCTCATGCGGCCCAGGTTCGGCATTTTGCTCACAGTCATCTCATGGTTCCTC
      AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 5    CACTCTCCCACACTTCTTCTGTGACTTGGCCCCTCTGCTCAAACTGTCCTGTTCAGATACAT
      TGATCAATGAGCTTGTGTTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTACACTC
      AGCTTCTTTTCCTATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTTCCACACAGGGAA
      AGTGGAAAGCCTTCTCCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
      CATTGTAGGCGTGTACTTTTTCCCCTCCTCCACTCACCCTGAGGACACTGATAAGATTGGT
 10   GCTGTCCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
      AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ
      ID NO: 2)
```

AOLFR2 sequences:

```
 15   MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIIIKINPKFHTPMYFFL
      SHLSFVDFCYSSIVTPKLLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
      NPLLYTVAMSQRLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPNVINHFFCEYTALISVSGS
      DILIPHLLLFSFATFNEMCTLLIILTSYVFIFVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTILFL
      YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 20   3)
```

```
      ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG
      ATTACCCAAAGCTTCAGATTCCTCTCTTCCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
      GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTTCACACTCCTATGT
 25   ACTTTTTCCTTAGTCACCTCTCTTTTGTTGATTTTTGTTACTCTTCCATTGTCACTCCCAAGC
      TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
      CTTCCTGTCCTGCACTGCTGTGGTGACAGAGTCTTTCTTGCTGGCAGTGATGGCCTATGAC
      CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG
      CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCCTTGGTACTCCTTTGTTAT
 30   GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC
      TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCCACCTGCTGCTTTTCAGCTTCGCCA
      CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCCTATGTTTTCATTTTTGTGACT
      GTACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCCACC
      TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCCTTTACTGTGTACCCAACTCCAAA
 35   AACTCTCGGCAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
      ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
      TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)
```

AOLFR3 sequences:

```
 40   MLLTDRNTSGTTFTLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ
      LSFVDFCYSSIIAPKMLVNLVVKDRTISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL
      LYTVDMSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSSLLSLSCSDTYI
      NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTILFLYCV
      PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)
```

```
 45
      ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTCACCCTCTTGGGCTTCTCAGATT
      ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTTCTGGCCATCTACAATGTCACTGTGCTA
      GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACTGCATACCCCCATGTACT
 50   TTTTCCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCCTCCATCATTGCTCCCAAGATG
      TTGGTGAACCTTGTTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT
      TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCGTATGACCGC
      TTCGTGGCCATTTGCAACCCTCTGCTCTACACAGTTGACATGTCCCAGAAACTCTGCGTGC
      TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCCTTGGAACTGACGTGCTCTGC
 55   TTTAAAGTTATGTTTTCATGGTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
      TACTCTCCCTTTCTTGCTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC
      TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
```

CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG
ACTGCCATCACCATCCTTCCATGGCACCATCCTCTTCCTTTACTGTGTGCCCAACTCCAAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC

5   ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS

10   LLDVMFSSVVAPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACTDTHILGL
LVTLNSGMMCVAIFLILIASYTVILCSLKSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC

15   TGTGGAAAATATTTTCTGCTGTGTTTCTTGTCATGTATGTAGCCACAGTGCTGGAAAATCT
ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTCACCTATGTATTTTTTTCTTA
CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCCCAAGGTGATTGTAGAC
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC

20   CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCCACGGGTGTGCTGCCTAATGGTA
GGAGGGGCTTGGGTGGGGGGATTTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA
TACCCTTCTGTGGTCCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCCTACACGGTCATCCTATGCTCCCTGAAGTCT

25   TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCCACCTCACGGTGGTTG
TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTCACCCCCATAGAC
AAGGCAATGGCTGTGTCAGACTCAATCATCACACCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAAACTCTGGATGAAATGGGAGGCTTTGG

30   CTGGGAAATAA (SEQ ID NO: 8)

AOLFR5 sequences:

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLLANLGMIALIQVSSRLHTPMYFFLSH

35   LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
ETLLFLVATLNESVTIMIILTSYLLILTTILKMGSAEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC

40   CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCCTTCTCATCTATGGAGTCACGTTGTTAGCC
AACCTGGGCATGATTGCACTGATTCAGGTCAGCTCTCGGCTCCACACCCCCATGTACTTTT
TCCTCAGCCACTTGTCCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCCTAGGGTGCATGGTGCAATTCTACT
TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT

45   GTGGCCATCTGTAACCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCATTTGTGCTTAGCTCTT
AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT
AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCCTGGTGGCCCACTTTG
AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT

50   GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCCAGTTCAGGCAATA
GTGGAGATGCTGACAAAGTGGCCACCGTGTTCTACACAGTCGTGATTCCTATGCTGAACTC
TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
CAAAATTCACTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
HLSLTDFCFSTVVTPKLLENLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCK
PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFICDHSVIVSASYSDPYIS
5　QRLCFIIAIFNEVSSLIIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTILFLYCVPNP
KTSSLIVTVASVFYTVAIPMLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCGGTCTACACAGTCACTGTA
10　GTGGGGAACTTGGGCATGATAATAATCATCAGACTCAATTCAAAACTCCATACAATCATGT
ACTTTTTCCTTAGTCACTTGTCCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTTCTCTGGTTGCATCATGCAAT
TTTGTTTTGCTTGCATTTTTGGAGTGACAGAAACTTTCATGTTAGCAGCGATGGCTTATGAC
CGTTTTGTGGCAGTTTGTAAACCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
15　TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACTTTCTCCACCTGTGCCTCCCACC
20　TGACAGCCATCACTATCTTCCATGGAACTATCCTTTTCCTTTACTGTGTTCCTAATCCTAAA
ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

25　**AOLFR7 sequences:**

MSYFYRLKLMKEAVLVKLPFTSLPLLLQTLSRKSRDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY
VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
30　FRVLLMSRLSFCASHIIKHFFCDTQPVLKLSCSDTSSSQMVVMTETLAVIVTPFLCIIFSYLRIMV
TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
PFIYSLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACTGCCCTTTA
CATCTCTCCCACTGCTTCTCCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
35　CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCTCAGCTGCAG
AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
CATCCCGGCCATCTACTCTGACCCCAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
TGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCCAGATGTACTTCTTTATGGCAT
40　TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
TCTTGCAGCATCTCCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGGCTTGTCTTT
CTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCATTGTGAC
45　CCCCTTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT
CTGCAGCCGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCCTGTCCATGTACTCAGTGGTTAGGG
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCTTTCATCTACAG
CCTGAGGAACAAAGATATGAAGAGGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
50　A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYYFLSH
LSFIDLCYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
55　NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMYFKPPSS
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

ATGGCTACTTCAAACCATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
5   CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCTTGGAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTCATTGATCTCTGCTACTCCTCTGTCATTACCCCTAAGATGCTG
GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
CTTCCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
10   GTTGCTATCTGTCGCCCACTGCTTTACAATATTGTCATGTCCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCATTATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT
15   TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTCATGTATTTCAAGCCCCCTTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFGLNSHLHTPMYYFLFN
LSFIDLCYSSVFTPKMLMNFVSKKNIISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
25   LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHYLCDILPLLQLSCTSTYV
NEVVVLIVVGTNITVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
SSGSMEQGKVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCTTCTTTTTCCTGTTCCTAGTGATCTACATTGTCACCATGGTAGGC
30   AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
TTTCTCTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
35   CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCACACCGGGTGCATGTTTAG
ACTCACCTTCTGCAGTGCTAATATCATTAACCATTACTTGTGTGACATACTCCCCCTCCTCC
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTCATTGTCACTAGCATTCTTC
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCTATGTCATTGC
40   TCTGTCTCTGTTTTTTGGGTCAGCGGCATTCATGTATATTAAATATTCTTCTGGATCTATGG
AGCAGGGAAAAGTTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCTCATC
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45   **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFNL
SFIDLCYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMLRLTFCSANIINHYLCDILPLLQLSCTSTYVN
50   EVVVLIVVGINIMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
SGSMEQGKVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTTTCCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
55   CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

-87-

```
     TTCTCTTTTTTGTCATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
     GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCAC
     TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCACACCGGGTGCATGCTTAGA
     CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
  5  GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
     ATCATGGTACCCAGTTGTACCATCCTCATTCTTTATGTTTTCATTGTCACTAGCATTCTTCA
     TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGCT
     CTGTCTCTGTTTTTGGGTCAGCGGCATTCATGTATTAATTAAATATTCTTCTGGATCTATGGA
     GCAGGGAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
  10 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGA
     GAAGAAATATATTCTAA (SEQ ID NO: 20)


     AOLFR11 sequences:

     MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS
  15 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPLLY
     MVTMSPRVCFLLMFGSYVVGFAGAMAHTGSMLRLTFCDSNVIDHYLCDVLPLLQLSCTSTHV
     SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSHIIAVALFFGSGTFTYLTTS
     FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)


  20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC
     CAGAGCTCCAGCTCCCTCTTTTCCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
     AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT
     CCTCTTCAACTTGTCCTTTATAGATCTCTGTTATTCCTGTGTGTTTACCCCCAAAATGCTGA
     ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
  25 TGTTTCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
     CATCTGCAACCCCCTGCTCTACATGGTCACCATGTCCCCAAGGGTCTGCTTTCTGCTGATGT
     TTGGTTCCTATGTGGTAGGGTTTGCTGGGGCCATGGCCCACACTGGAAGCATGCTGCGACT
     GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC
     TCTCCTGCACCAGCACCCATGTCAGTGAGCTGGTATTTTTCATTGTTGTTGGAGTAATCACC
  30 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGTTGATCTCTCCAACATCCTCTGTATT
     TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCCACATAATTGCTGTT
     GCTCTGTTTTTTGGGTCAGGGACATTCACCTACTTAACCAACATCTTTTCCTGGCTCTATGAA
     CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCTTCGATCT
     ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAAACCCTGAAGAGAGTGCTCT
  35 TCTAA (SEQ ID NO: 22)


     AOLFR12 sequences:

     MERNHNPDNCNVLNFFFADKKNKRRNFGQIVSDVGRICYSVSLSLGEPTTMGRNNLTRPSEFIL
  40 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLIILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
     NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMAIDRYVAICNPFHYITIMSHRCCVLLLVLS
     FCIPHFHSLLHILLTNQLIFCASNVIHHFFCDDQPVLKLSCSSHFVKEITVMTEGLAVIMTPFSCIII
     SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
     MLNPFIYSLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)


  45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA
     AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
     TTAGTTTATCTTTAGGTGAACCCACAACTATGGGAAGAAATAACCTAACAAGACCCTCTGA
     ATTCATCCTTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
     TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
  50 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTTGACATTTGCT
     ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACTTCTTATCAGAGACAAAGACCATCTC
     TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
     CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
     CCATTATGAGTCACAGATGCTGTGTCCTGCTTCTCCTTGTCCTGTCATTCTGCATTCCACATTTT
  55 CACTCCCTCCTGCCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
     TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCCTGTTCCTCCCATTTTGTCAAAG
```

-88-

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTCATGCATCATCAT
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCTTCAGCTGCTGGAAAGCGTAAA
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA
TGTCTATTTTCAGCCCCTGTCCAACTATACTGTCAAGGATCAAATAGCAACAATTATCTAC
ACCGTACTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

MDQKNGSSFTGFILLGFSDRPQLELVLFVVLLIFYIFTLLGNKTIIVLSHLDPHLHNPMYFFFSNL
SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
HYTVVMHPCLYVLMASTSWVIGFANSLLQTVLILLTLCGRNKLEHFLCEVPPLLKLACVDTT
MNESELFFVSVIILLVPVALIIFSYSQIVRAVVRIKSATGQRKVFGTCGSHLTVVSLFYGTAIYAY
LQPGNNYSQDQGKXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTcTTTGATCTTCTATATCTTCGCTCTTTGCTGGGG
AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTCAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTTGACCGCTAT
GCAGCTGTTTGCAGGCCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCTCCATTGCT
CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACTCTTCTTTGTCAGTGTCATTA
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCCACCTCACA
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAACTACTC
TCAGGATCAGGGCAAGKTCATCTCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA(SEQ ID NO: 26)

AOLFR14 sequences:

MALPLLLSPSCFASSQSLSSRMNSENLTRAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLLPRATIPYTACALQMF
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF
RLSFCRSRKINSFFCDIPPLLAISCSDTSLNELLLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACTCAGAGAACCTCACCCGGGCCGGCGGTGCCCCTGCTGAATTCGTCCTCCTGGGC
ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCCTGACCTGCCTGCCTGTCTACCTGG.
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCGGCTCCACA
CACCTATGTACTTCTTCCTGGCCAACCTCTCCCTGCTGGATGCCTGCTGGTTGCCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
CCCTCCACGATGTTTGTCTTTGCAGGTCTGGCTGGTGATACTGAGTGGTTGCTGGCCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTCGCAG
CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGGCCTTTGTTC
ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCAGTCTCAATGAACTCCTTCCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTCGAGGGCAGTCGGCGAGCAGCCTCCAC
CGGTGGTTCCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

5   MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNPMYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLLKLSCSDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR
PLTNYSLKDAVITVMYTAVTPMLNPFIYSLRNRDMKAALRKLFNKRISS (SEQ ID NO: 29)

10

ATGAGGGAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTTCCTGTTTCATTTACCCCATCACATTGATTGGA
AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTCGCCTTCACAACCCCATGTATTTTCT
CCTTGCCAACCATCTCCTTGGTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
15   CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTGCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCCACACTCTGCTCACAGC
TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGGCCAACTTCTACTGTGACATTACCCCCTTG
20   CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCCACCTCACGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTCAT
25   CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMVTVAGNLGMIVLIQANAWLHMPMYFFLSH
30   LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVQCYLFIALVHVEIYILAVMAFDRYMAICNPLL
YGSRMSKSVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINHFYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGKMVAVFYTTVIPMLNLIIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35   ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCTCCTCTTCACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
AGATTTTCCTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCAGTGTTACCTT
40   TTTATCGCCTTGGCTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC
ATCACGGTCCCTTATGTGTATGGAGCGCTACCTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
TAAGCTGGCTTGTTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
45   AACCTTTCTTTTTCTCTCTTCATCATATGTATTTCCTACCTTTACATTTTCCCTGCTATTTTA
AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
50   AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIIFLVVYIITMVGNIGMMVLIKVSPQLNNPMYFFLSHLS
55   FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL
YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINHFYCADPPLIKMACAGTFVKE

-90-

YTMIILAGINFTYSLTVIIISYLFILIAILRMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGKMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5
ATGCTCAATTTCACCGATGTGACAGAGTTCATTCTTTTGGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTTCCTCA
GTCACTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTCAGATAAAAAAACAATTACTTATGCTGGTTGTTAGTACAGTGTTTCTTCTTCAT
TGCTCTTGTCCATGTGGAAATTTTTATTCTTGCTGCGATGGCCTTTGATAGATACATGGCAA
TTGGGAATCCTCTGCTTTATGCAGTAAAATGTCAAGGGTTGTCTGTATTCGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACTTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCTCATTGCCATTCTGCGAAT
GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTTAA (SEQ ID NO: 34)

20

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLLFVLFLVVYLVTLLGNLGMIMLRLDSRLHTPMYFFLT
NLAFVDLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
EHAMFISAGFNLSSSLTIVLVSYAFILAAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAACTCCAGTCTCTGCTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATTA
AGCTTTCTTGTTCTGATACTTATGTCAAAGAGCATGCCCATGTTCATATCTGCTGGTCTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCCTATGCCTTCATTCTTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
TGTCACCCTGTTTTATGGGACTCTCTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPKLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYPMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRLSFCASHIIKHFFCDTQPVLKLSCSDTSSSQ
MVVMTETLAVIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFR
PLSMYSVMKGRVATVMYTVVTPMLNPFIYSLRNKDMKRGLKKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCCAGGCTCCACACCCCTATGTACT
TTTTTCTCAGCAACTTGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATG
CTGGTGAATTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
CTCATGCTATTGGGTTCTTGCAGCATCTCCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACCACCCAGCCTG
5   TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
AGCTGTCATTGTGACCCCCTTCCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
TGCTCAGAATCCCCTCTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCT
CACTGTAGTGGTCCTGTTCTATGGGAGTGTCATCTATGTCTATTTAGGCCTCTGTCCATGT
ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGTGA
10   ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

15   MVEENHTMKNEFILTGFTDHPELKTLLFVVFFAIYLITVVGNISLVALIFTHCRLHTPMYIFLGN
LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPYLRLSCVDPF
INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
NLLEEGGNDIPAAILFTTVVPLLNPFIYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

20   ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
CTGAGCTGAAGACTCTGCTGTTTGTGGTGTTCTTTGCCATCTATCTGATCACCGTGGTGGG
GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC
TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGCTGTGCCTGTGCTATTACCCCCAAAATGTT
25   AGAGAACTTCTTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
TTTCTTTGCACTGTGGAAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAAACTCTGCATTCA
GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTCATGTAGGGCTTGTA
TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
30   GTATAGACTCTCCTGTGTTGACCCTTTCATCAATGAACTGGTTCTATTCATCTTCTCAGGTT
CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT
TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTCTACTTGTGCATCCCACTTTT
CATCAGTTTCATTATTCTATGGATCTATTTTTTCCTATACATTAGACCAAATTTGCTTGAA
GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCCTTACTAAATC
35   CTTTCATTTATATGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDFVLLGFTQNPKEQKVLFVMFLLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
40   TFIDIIYSSSISPRLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV
IMRQWVCVLLLVVSWVGGFLQSVFQLSIIYGLPFCGPNVDLHFFCDMYPLLKLACTDTHVIGLL
VVANGGLSCTIAFLLLLISYGVILHSLKKLSQKGRQKAHSTCSSHITVVVFFFVPCIFMCARPAR
TFSIDKSVSVFYTVTITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCCTCTTGGGCTTCACACAGAATCCAAAG
45   GAGCAGAAAGTACTTTTTGTTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
GCTCATTGTAGTGACCGTAACTGTCAGTGAGACCCTGGGCTCACCAATGTCCTTCTTTCTT
GCTGGCTTAACATTTATAGATATCATTTATTCTTCATCCATTTCCCCCAGATTGATTTCAGA
CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCCAGCTCTTTATCGAGC
ACCTTTTTGGTGGTCAGAGGTCTTTCTCCTGTTGGTGGTGATGGCCTATGACCGCTATGTGGC
50   CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTTGCTGCTG
GTAGTGTCCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
TCCCATTCTGTGGCCCCAATGTCATTGATCATTTTTCTGTGACATGTATCCCTTATTGAAA
CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTCATCCTGCACTCTCTAAAGAAA
55   CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCCACATCACTGTGGTTG
TCTTCTTCTTTGTTCCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

-92-

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5   MRXXNNXTEFVLLGFSQDPGVXKALFVMFLLTYXXTVVGNLLIVVDIIASPXLGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQGCMGQLFIDHFFGGAEVFLLVVMACDRYVAICKPL
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI
GLTVVVNSGAICMVIFNLLLISYGVILSSLKTYSQEKRGKALSTCSSGSTVVVLFFVPCIFIYVRP
VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:

10   43)

ATGAGACANNNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTCATGTTTTTACTCACATACNNNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCCCAATGTATTTCTTCCTTG
CCTGCCTGTCATTTATAGATGCTGCATATTCCACTACCATTTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
ATTTCTTTGGTGGGGCTGAGGTCTTCCTCTTTGGTGGTGATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCCTTCTGTTGG
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCATTTCAAATTGTTGTTGTTCTGTACAGTCTCCCT
TTCTGTGGTCCCNATGTCATTGTTCATTTCAGTTGTGACATGCACCCATTACTGGAACTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAAACTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCCTC
TTTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACTTTCCTACTGATAAGTT
CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTGGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAATGCTATAGAAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30   MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLFTICAGTECFLLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFFCDLPPLLKLACSDTA
NIEIVIFFGNFVILANASVILISYLLIIKTILKVKSSGGRAKTFSTCASHITAVALFFGALIFMYLQS
GSGKSLEEDKVVSVFYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
CCAAATTGGAGATTCCCCTCTTTCTGGTGTTTCTGAGTTTCTACCTAGTCACCCTTCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACTCTACACCCCAATGTACTTCT
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA
GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCCAGTTCTTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
TGCTGCCATTCGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTCAGGAGCCATCCTGCGTACCACTTGCACCT
TCACCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCCTATCTGCTCATCATCAAGACCATT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCTTCCCATCACA
CTGCTGTGGCCCTTTTCTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
CTCTGATCTCACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55   METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIIITVTSDSQLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMGQIFFFHFLGGAMVFFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLRLACTDT

SLLEFLKISNSGLLDVVWFFLLLMSYLFILVMLRSHPGEARRKAASTCTTHIIVVSMIFVPSIYLY
ARPFTPFPMDKLVSIGHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTTCCTGTTTCTAATGTTCCTGTTTGTCTACATCACCACTGTTATGGGA
AACATCCTTATCATCATCACAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
GCTCCGAAACCTGGCTGTCCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAAATGCTAG
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTCAGATCTTCTT
CTTCCACTTTTGGGAGGTGCCATGGTCTTCTTCCTCTCAGTGATGGCCTTTGACCGGCTCA
TTGCCATCTCCCGGCCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
CCACTGCCCTTCTGTGGCCCCAACATTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
GAGACTTGCCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
CTGGATGTCGTCTGGTTCTTCCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA
TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
LIDFCFSTTITPKMLMSFVSRKNIISFTGCMTQLFFFCFFVVSESFILSAMAYDRYVAICNPLLYT
VTMSCQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPLLELSCNSSYMN
ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
LSILPLEQGKVSSLFYTIIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
GACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
CCTGGGCTTGATAACCCTCATTGGGCTGAACTCTCACCTGCACACTCCCATGTACTTCTTCC
TTTTTAACCTCTCTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
AGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAGCTCTTCTTCTT
CTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTATGACCGCTACGTGG
CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCCACACAGGAAGCATAATGAAC
CTGACCTTCTGTGCTGACAACCTTGTCAATCATTTCATGTGTGACATCCTTCCTCTCCTTGA
GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
GTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAGTTCCCACACTAATTGTA
GTTTCTCTTTTCTTGGTTCTGGTGCTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCCTC
GAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

MPSQNYSIISEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIEHRLHTPMYLFLCTL
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHHFFCHVLSLLKLACENKT
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
LKPKGLHSMYSDALMATTYTVFTPFLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
51)

ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
CCAGCAACCTCCTGCCCATCTTGTTCCTGCTGTACCTCCTGATGTTCCTGTTCACATTGCTGG
GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTTGTGCACCCTCTCTGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

```
TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCAGATGTTC
TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCCTTCTCCTGGTCATGGGCTATGATCGCTA
TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGACTGTGCCCAT
CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTTCTGTCATGTGCTTTCCCTCT
TGAAGTTGGCCTGTGAAAACAAGACATCACTCATGACTGGGTGTGATGCTGGTGTGTGT
CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA
TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCCACCT
CACTGTGGTGGTCACGCACTATAGTTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC
ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCCTTCCTTAGC
CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTTACA
GAAAATTCTGTCCTCCAAGTTCCTGA (SEQ ID NO: 52)
```

AOLFR28 sequences:

```
MPNFTDVTEFTLLGLTCRQELQVLFFVVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSF
ADVCFSSNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVEVYILAVMAFDRYMAGCXPLL
YGSKMSRTVCVRLISVXYXYGFSVSLICTLWTYGLYFCGNFEINHFYCADPPLIQIACGRVHIKE
ITMIVIAGINFTYSLSVVLISYTLIVVAVLRMRSADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
RPTEESVEQGKMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)
```

```
ATGCCTAATTTCACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC
TACAGGTTCTCTTTTTTGTGGTGTTCCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT
GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTTCTGAG
TCATCTGTCTTTTGCGGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATGCTGGAAAACT
TATTATCAGAGACAAAAACCATTTCCTATGTGGGATGCTTGGTGCAGTGCTACTTTTTCAT
TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCGGCTCATCT
CTGTGNNNTATGNNTATGGATTCTCTGTCAGCCTAAATATGCACACTATGGACTTATGGCTT
ATACTTCTGTGGAAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACTT
CACATATTCCCTCTCGGTGGTCCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA
TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
TTCTATGTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT
ATGTGAGGCAGTAA (SEQ ID NO: 54)
```

AOLFR29 sequences:

```
MMSFAPNASHSPVFLLLGFSRANISYTLLFFLFLAIYLTTILGNVTLVLLISWDSRLHSPMYYLLR
GLSVIDMGLSTVTLPQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
PLHYALVMNHQRCACLLALSWVVSILHTMLRVGLVLPLCWTGDAGGNVNLPHFFCDHRPLLR
ASCSDIHSNELAIFFEGGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRRAVSTCGSHLTMVGFL
YGTIICVYFQPPFQNSQYQDMVASVMYTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP
(SEQ ID NO: 55)
```

```
ATGATGAGCTTTGCCCCTAATGCTTCACACTCTCCGGTTTTTTTGCTCCTTGGGTTCTCGAG
AGCTAACATCTCCTACACTCTCCTCTTCCTTTCCTGTTCCTGGCTATTTACCTGACCACCATAC
TGGGGAATGTGACACTGGTGCTGCTCATCTCCTGGGACTCCAGACTGCACTCACCCATGTA
TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCCAG
TTGCTGGCCCATTGGTCTCTCATTACCCAACCATTCCTGCTGCCCGCTGCTTGGCTCAGTT
CTTTTTCTTCTATGCATGTTGGGGTTACAGATACTTTGTCATTGCTGTCATGGCTCTGGATC
GCTATGTGGCCATCTGTGACCCCCTGCACTATGCTTTGGTAATGAATCACCAACGGTGTGC
CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC
GTCCTGCCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCCTCACTTCTTTTG
TGACCACCGGCCACTTCTGCGAGCCTCTTGTTCTGACATACATTCTAATGAGCTGGCCATA
TTCTTTGAGGGTGGCTTCCTTATGCTGGGCCCCTGTGCCCTCATTGTACTCTCTTATGTCCG
```

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCGCGCCGAGCAGTCTCCACC
TGTGGATCCCACCTCACCATGGTTGGTTTCCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACTCT
5   GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTIVGNLGMIT
LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNIISYAGCMSQLYFFLVFVIAEC
10   YMLTVMAYDRYVXXCHPLLYNIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY
FCDILPLMKLSCSSTYDVEMTVFFSAGFNIIVTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHL
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGK
LF (SEQ ID NO: 57)

15   ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
GAAATCACTCTACAGTGACAGAGTTCATTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
AGCTCCCCCTCTTTCTCCTCTTCCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC
ATGATCACTCTAATTTGTCTGAACTCTCAGCTGCACACCCCCATGTACTACTTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACTTTG
20   TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCCTTGT
TTTTGTCATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
TGCCACCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAAACTGGCCTCATGTTAAAACTGCCC
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCCTG
25   CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC
ACGAGCTTAACAGTTCTTGTTTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGCAGCCGTGGGAAT
GTTCTATGGATCAACTGCATTCATGTACTTAAAACCCTCCACAATCAGTTCCTTGACCCAG
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
30   GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
GA (SEQ ID NO: 58)

AOLFR31 sequences:

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIVLRRSHHLHTPMYIFLCHL
35   AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLLAAMAYDRYVAICSP
LLYSTCMSPGVCIILVGMSYLGGCVNAWTFIGCLLRLSFCGPNKVNHFFCDYSPLLKLACSHDF
TFEIIPAISSGSIIVATVCVIAISYIYILITILKMSHTKGRHKAFSTCTSHLTAVTLFYGTITFIYVMP
KSSYSTDQNKVVSVFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40   ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
CTACAGTTTGTGCTATTTTTATTTCTTGTGTGTTCTAGGGAATTTATGTTGTCACCTTAATGGGT
AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT
TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCCAGCTCTGTT
45   CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCCTGCTGGCTGCCATTGCATGGTGCTTATT
TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCTGGAGTCTGCATCATCT
TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAACGCTTGGACATTCATTGGCTGCTTATT
AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACCACTTT
TGAAGCTTGCTTGTTCCCATGATTTTACTTTTGAAAATAATTCCAGCTATCTCTTCTGGATCT
50   ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
GAAGATGCACTCCACCAAGGGCGGCACAAGGGCCTTCTCCACCTGCACCTCCCACCTCACT
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
55   AAAATATTTTCTTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAAFFATVECVLLAAMAYDRFVAICSPLLYSTK
5   MSTQVSVQLLLVVYIAGFLIAVSYTTSFYFLLFCGPNQVNHFFCDFAPLLELSCSDLSVSTVVLSF
SSGSIIVVTVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
DQNKVVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
NO: 61)

ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
10 CAGATGATCCAATCCTTGGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
GGCTTTTGCTGACATGGCCTATTCATCTTCTGTCACACCCAACATGCTTGTAAACTTCCTGG
TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGGCTTTGTGGCAATTTGC
15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
TTTACATAGCTGGTTTTCTCATTGCTGTCCTATACTACTTCCTTCTATTTTTTACTCTTCT
GTGGACCAAATCAAGTCAATCATTTTTTCTGTGATTCGCTCCCTTACTTGAACTCTCCTGT
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCTCATTTCTTCTGGATCCATCATTGTGGTCAC
TGTGTGTGTCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
20 CTGAGGGGCACCACAAGGCCTTCTCCACCTGCACTTCCCATCTAACCTGTGGTTACCCTGTT
CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCCTGATCTACAGCC
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

AOLFR34 sequences:

MLEGVEHLLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPPQLGAPLFLAFLVIYLLTVSGNG
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHFLGCT
30 ECFLYTLMAYDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVFRLPFCGPNRV
DYIFCDIPAMLRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST
CAAHLTVVIVYYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIIYTLCNKEMKAALQRLGG
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
35 AACTGCAAAGTGGAAACCAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCACCC
ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCCTTGTCATCTATCTCCTCACTGTTTCTG
GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
GTTCCTGTGTCACCTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCCAAGATGC
TGGCTGGCTTTCTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACTATTT
40 TCTTTCCATTTCCTGGGCTGTACTGAGTGCTTCCTTTACACACTCATGGCTTATGACCGTTT
CCTTGCCATTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCGTGTAACTCCC
TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTTGTATT
CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCCTGCCATGC
TGCGTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGTGGTCACCTTTGCAGACATTGGCTT
45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCCTATGGCTATATTGTAGCTGCCATCC
TGCGAATTCCGTCAGCAGATGGGCGCCGCAATGCCTTCTCCACTTGTGCTGCCCCACCTCAC
TGTTGTCATTGTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTCACAGGAGC
CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTCATCACTCCCTTGCTTAACTCCATCATC
TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGFSGYPALEHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG
NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLLAITAYDRYLAICQPL
55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTEMVISMRLPFCGHHVVSHFTCKILAVLKLACGNT
SVSEDFLLAGSILLLPVPLAFICLSYLLILATILRVPSAARCCKAFSTCLAHLAVVLLFYGTIIFMY

-97-

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
5 CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCTCCTGGG
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACCACGCCCGTGTACTTC
TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCCACCTTTGTGCCTCTGATGCT
GGTCCACCTCCTGTCATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
TGAGCCTGTCCACGGGCTCCACGGAGTGCCTGCTACTGGCCATCACGGCCCTATGACCGCTA
10 CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG
CTGATGGGAGCTGCCTGGGTCCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
GCTGAAGCTGGCATGCGGCAACACGTCGGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT
CCTGCTGCTGCCGTGTACCCCTGGCATTCATCTGCTGTCCTACTTGCTCATCCTGGCCACCA
15 TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG
GAAGCCCACATCTCTGATGAGGTCTTCACAGTCCTCTATGCCATGGTCACGACCATGCTGA
ACCCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

AOLFR36 sequences:

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
WIVLQFTFFKNVEISNFVCEPSQLLKLASYDSVINSIFIYFDNTMFGFLPISGILLSYYKIVPSILRIS
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFIYS
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC
ACCCCCACACACCCATGTACTTCTTCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
30 TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCCT
GACTGTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC
GTGAATCCTCACCTCTGTGTCTTCTTGTTTTGGTGTCCTTTTTCCTTAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT
35 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCTCTTATGACAGCGTCATCAATAGCATA
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC
TATAAAATTGTCCCCTCCATTCTAAGGATTTCATCATCAGATGGGAAGTACAAAGCCTTCT
CAGCCTGTGGCTGTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
40 GTGGTCACCCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCTTAG
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**

MEKANETSPVMGFVLLRLSAHPELEKTFFVLILLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSFLTPQETISFSACAVQMALSFAMAGTECLLLSMMAFDRYVAICNP
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFIITTILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
50 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKAAVRRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGGT
55 GGGCAATGGGGTCCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC
TTCTTCCTAGGGAACCTCTCCTTCCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

```
          CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
          GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTTGATC
          GCTATGTGGCCATCTGCAACCCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
          GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTGGTACACACATCCTTG
     5    GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
          CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
          TGTGATCTTCCTAGGAGTCCCGGTTCTGTTCATCTCTTTCTCCTATGTCTTCATCATCACCA
          CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
          CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
     10   AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACATCATCCCCCTTTTCTATG
          GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
          CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)
```

AOLFR38 sequences:

```
          MYLVTVLRNLLIILAVSSDSHLHTPMCFFLSNLCWADIGFTSAMVPKMIVDMQSHSRVISYAGC
          LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVFLVLVSFFLSLLDSQLHSW
          IVLQFTFFKNVEISNFVCDPSQLLNLACSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS
          SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFIYSLR
          NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)
```

```
          ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
          ACCTCCACACCCCCATGTGCTTCTTCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
          TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
     25   CGGGCTGCCTGACACAGATGTCTTTCTTTGTCCTTTTTGCATGTATAGAAGACATGCTCCTG
          ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCCTGCACTACCCAGTCATCA
          TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCCTTTTTCCTCAGCCTGTTGGATTCC
          CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCCAATT
          TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCCTGTTCTGACAGTGTCATCAATAGCATA
     30   TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC
          GCTAACAATGTCCCCTCCATTCTAAGAATTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
          CCACCTGTGGCTCTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
          CCTGACTTCAGCTGTGTCACCACCCCCCAGGAATGGTGTGGGGTGGTGGCTCAGTGATGTACGCT
          GTGGTCACCCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
     35   CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
          CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)
```

AOLFR39 sequences:

```
          MGVKNHSTVTEFLLSGLTEQAELQLPLFCLFLGIYTVTVVGNLSMISIIRLNRQLHTPMYYFLSS
          LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVCVISECYMLAAMACDRYVAICSPL
     40   LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIIKHYFCDIVPLIKLSCSSTYIDEL
          LIFVIGGFNMVATSLTIIISYAFILTSILRIHSKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
          SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)
```

```
          ATGGGTGTAAAAAACCATTCCACAGTGACTGAGTTTCTTCTTTCAGGATTAACTGAACAAG
     45   CAGAGCTTCAGCTGCCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
          AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCCATGTACTAT
          TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCATTACCCCTAAAATGCT
          ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTT
          TTTTCTGTGTTTGTGTTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
     50   GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
          TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGGTGTATACT
          CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA
          TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCATTGGTGGATTT
          AACATGGTGGCCCACAAGCCTAACAATCATTATTTCATATGCTTTTATCCTCACCAGCATCCT
     55   GCGCATCCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCCACCTGACA
          GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCCAGTTC
```

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMLTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTS
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
10 RPGSRDALHGVVAVFYTTLTPLFNPVVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCCTGGGGAGCACCGAGTGTTTCCTCTACACAGTCATGTCCTATGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAACAATGATGACTGAGGCCTCGTGTGCCCTCCTG
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATGTGTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
25 GTGGTCCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT
TTGCTCAGGGTGAATAG(SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSSHLIQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTGDHTISFVSCIIQSYLYFFLGTTDFFLLAVMSLDRYLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNGIDHFFRDSWPLLRLSCGDTH
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAAERRKAFSTCASHLTVVVIIYGSSIFLY
35 IRMSEAQSKLLNKGASVLSCIITPLLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAACTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC
TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC
TCTACTTCTTTCTAGGCACCACTGACTTCTTCCTCTTGGCCGTCATGTCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCCTCTGGGTCCTTTGCCCCACTGTCCTCATGGGC
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
CAGGCTTTCTTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTCATGCTCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCCTATGCCTGCATTCTTGCCACTGTTCT
CAGGGCCCCTACAGCTGCTGAGCGAAGGAAAGACGTTTTCCACTTGCGCCTCGGCATCTTACA
50 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTC
CAAACTGCTCAACAAAGGTGCCTCCGTCTCTGAGCTGCATCATCACACCCCTCTTGAACCCA
TTCATCTTCACTCTTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

55

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFFHFIGGKIFLLTVMAYDRYIAISQPL
HYTLIMNQTVCALLMAASWVGGFIHSIVQIALTIQLPFCGPDKLDNFYCDVPQLIKLACTDTFV
5   LELLMVSNNGLVTLMCFLVLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
TRPFRTFPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
(SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
10   GGGAGCTTCGGTTTGTGTTTCTTCACTGTTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
CTTGGGCAATCTTTCTTTCCTGGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG
TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCTGACTCAACTCTTCTTC
TTCCACTTCATTGGAGGCATCAAGATCTTCCTGCTGACTGTCATGGCGTATGACCGGCTACA
15   TGCCATTTCCCAGCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACTTTTATTGTGATGTGCCTCAGCTGAT
CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTHAACAATGGCCTG
GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
20   GAAGCCACTCACGGGAGGGCCGCAGCAAGGCCCTGTCTACCTGTGACCTCTCACATTGCTGT
GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATACAAGGCCTTTTCGGACATTCCCCA
TGGACAAGGCCGTCTCTGTGCTATACACAATTGTCACCCCCATGCTGAATCCTGCCATCTA
TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

25   AOLFR43 sequences:

MQKPQLLVPIIATSNGNLVHAAYFLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHALSAVESAVLLA
MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFFPLPFILKWLSYCQTHTVTHSFCLHQ
30   DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV
LVFYVPLIGLSVVHRLGGPTSLLHVVMANTYLLLPPVVNPLVYGAKTKEICSRVLCMFSQGGK
(SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
35   CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT
TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCCTGGCCATGCTTTCCACTATT
GACCTAGTCCTCCTCTCTATCACCATGCCCAAGATGGCCAGTCTTTTCCTGATGGGCATCCA
GGAGATCGAGTTCAACATTTGCCTGGCCCAGATGTTCCTTATCCATGCTCTGTCAGCCGTG
40   GAGTCAGCTGTCCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC
GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCCTACTGCCAAACAC
ATACTGTCACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCCTGTACTGACAC
CAGGGTCAATGTGGTTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
45   TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTGGAGCTGTCCTCTCGGAGGGCA
GCACTCAAGGCTTTCAACACCTGCATCTCCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT
ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCCTTGTCTATGGAGCCAAGA
CCAAAGAGATCTGTTCAAGGGTCCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
50   NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFIHALSAIESTILLAMAFDRYVAICHPL
55   RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
NVVYGLTAILLVMGVDVMFISLSYFLIRTVLQLPSKSERAKAFGTCVSHIGVVLAFYVPLIGLS

-101-

VVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTTCTGGGTTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGCAATGTTTGGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTGACCGTTATGTGG
CCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTCATCTCCTTGTGTCCTATTTTCTGATAATACGAACGGTTCTGC
AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTCACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
CTTCATCCCATTGTGCGTGTTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA
MLATIDLVLSSTTLPKMLAIFWFRDQEINFFACLVQMFFLHSFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMTPLPFLLRRFHYCRGPVIAHCYCEHMAVVRLACGDT
SFNNIYGIAVAMFSVVLDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTTGTTGGTAGGAAT
TCCTGGTTTGGAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCTTCTCTTCATTATCCAGGTCTGATGCAGCCTCCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC
CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGACTACACGACGGTCCTGACTGGGTCCCTC
ATCACCAAGATTGGCATGGCTGCTGTGGCCGGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCCAGGCCCAGTGATTGCCCATTGCTACTGTGAACA
CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT
TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTTGGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCGCCATGCTGCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCGTGAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
ATCTTTGACAATTCTCTAGTATGATAAGGAAAATGAGGTTTCATTCCTCACAGATCTACGA
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
TTGTCATAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

MNIKHCGWHMIHTWLNIREDDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLLICFPNFQSWQHWLSLPLSLLFLLAMGANTTLLITIQLEAS

LHQPLYYLLSLLSLLDIVLCLTVIPKVLAIFWFDLRSISFPACFLQMFIMNSFLTMESCTFMVMA
YDRYVAICHPLRYPSIITDQFVARAVVFVIARNAFVSLPVPMLSARLRYCAGNIIKNCICSNLSVS
KLSCDDITFNQLYQFVAGWTLLGSDLILIVISYSFILKVVLRIKAEGAVAKALSTCGSHFILILFFS
TVLLVLVITNLARKRIPPDVPILLNILHHLIPPALNPIVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
5   87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
10   TGGGTCTCCAGATTGATCANGAAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCTCAGCCTTCTCTTCCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
ACATCGTGGCTCTGGCTCCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
15   TCGATCAGCTTCCCAGCCTGCTTCCTCCAGATGTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTCTCTTCCTGTTCCCACGGCTCTGGTTGGGCTCTGATCTTATCCTT
20   CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCCATTGTTTATGGTGTGAGA
25   ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIIQADAALHEPMYLFLA
MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
30   PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLLRCFHYCRGPVIAHCYCEHMAVVRLACGD
TSFNNIYGIAVAMFIVVLDLLLVILSYFILQAVLLLASQBARYKAFGTCVSHIGAILAFYTTVVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

35   ATGTCAGCCTCCAATATCACCTTAACACATCCAACTGCCTTCTTGTTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGGAAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCCTCCTCAGCACTGCCCAAA
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCCAGA
40   TGTTCTTCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA
CCAAGATTGGCATGGCTGCTGTGGCCCGAGCAGTCACTAATGACTCCACTCCCCTTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
45   CCATGTTTATTGTGGTGTTGGACCTGCTCCTTGTTATCCTGTCTTATATCTTTATTCTTCAG
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAACTGTGGTCATCTCTTCAGTCATGCACCGTGTA
GCCCGCCATGCTGCCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCAATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
50   GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYVAICH
55   PLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVATHASEP (SEQ ID NO: 91)

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACGAGCTCGATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCCCATGGCTTTT
GACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGCGGGGGCTGCACTGATGGCACCCCTTCCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCAGGTCAATGTCGTCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
AGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA
TGTGTGTGCTGTGTTCATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTA
GCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAAGGAGATTCGACAGCGCATCCTTCGA
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

AOLFR49 sequences:

MLTFHNVCSVPSSFWLTGIPGLESLHVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHCFATVESGIFLAMAFDRYVAIC
NPLRHSMVLTYTVVGRLGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTLGTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVHTLLANFYLLIPPILNPIVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID NO: 93)

ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGCTGACATTGGCCTGGACGCCTGCTTGGGCCAA
ATGTTCCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCTTGCCATGGCTTTGA
TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTTTCTCTCCTCCGGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCCTGCGGCTGCCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAAACCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTGCTGTTTCTTCCCTGATTCACCG
ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

AOLFR50 sequences:

MNLDSFFSFLLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFLSMLAAIDLVVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLLIPFLILLRKLIFCQATIIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGLDVLAIGVSYAHILQAVLKVPGNEARLKAFST
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVHVLLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

ATGAAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCCAGCCTTCTTTTTTCCTGGTAGGAATTCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCCTGTCC
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC
TCCTGGTTCGTGCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
5   TTTGTCACCCCTTGCACCATTCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
GGTGGTGCTGGTGCGGGGATTACTACCTCCTCATCCCCTTCCTCATTCTGTTGCGAAAACTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
TGGGCTGGATGTCCTGGCCATTGGTGTTTCCTATGCCCACATTCTCCAGGCAGTGCTGAAG
10 GTACCAGGAAATGAGGCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCCTCACTCACCGCTTTGGTCATCATGTA
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**
MCQQILRDCILLIHHLCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM
YIIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQ
MFFVHLATAVETGLLLTMAFDRYVAICKPLHYKRILTPQVMLGMSMAITIRAIIAITPLSWMVS
HLPFCGSNVVVHSYCEHIALARLACADPVPSSLYSLIGSSLMVGSDVAFIAASYLILLKAVFGLSS
20 KTAQLKALSTCGSHVGVMALYYLPGMASIYAAWLGQDVVPLHTQVLLADLYVIIPATLNPIIY
GMRTKQLRERIWSYLMHVLFDHSNLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
25 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGGAAACACCATCATCGTGACTGCCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCCTCACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGCACACCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
40 CTGGGTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:
MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY
CFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQMFFVHLATAVETGLLLTMAFDRYV
45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPFCGSNVVVHSYCKHIALAR
LACADPVPSSLYSLIGSSLMVGSDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMALY
YLPGMASIYAAWLGQDIVPLHTQVLLADLYVIIPATLNPIIYGMRTKQLLEGIWSYLMHFLFDH
SNLGS (SEQ ID NO: 99)

50 ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTTGTGGGTA
TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
AGCCCTGTTAGGGAAACACCCTCATCGTGACTGCCAATCTGGATGGATTCCACTCGGCATGAG
CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCGTGGT
ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTTC
55 ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
CTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

-105-

```
    AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG
    AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
    GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCAGCAGTCTCTACAGTCTG
    ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
5   TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAGCACATGT
    GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
    CCTGGTTGGGGCAGGATATAGTGCCCTTGCACACCCAAGTGCTGCTAGCTGACCTGTACGT
    GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAAACAATTGCTGGAG
    GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTCATGA (SEQ
10  ID NO: 100)


    AOLFR54 sequences:
    MSDSNLSDNHLPDTTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
    LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
15  ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGIARLACA
    NITVNIVYGLTVALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGIILVFYIPAFF
    SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLLKLLHLGKTSI (SEQ ID
    NO: 101)


20  ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
    CAGGGCTGGAGGCTGCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
    ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTCTTCATGCACCT
    ATGTACCTCTTCCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
    CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC
25  CAGATGTTTTGTGTGCCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT
    TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCTCAACCATGCTGTC
    ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
    CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTCATGACACACACATACTGTGAGCAT
    ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
30  TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTCCTATGGGCTTTATCCTC
    CATGCAGTCTTTCACCTTCCATCTCATGATGCCCAGCACAAAGCTCTGAGTACCTGTGGCT
    CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCTCACCCACCGC
    TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
    TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTCGGAGTCGACT
35  TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)


    AOLFR57 sequences:
    MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNIEVLCFVLFLFCYIAIWMGNLLIMISITCTQ
    LIHQPMYFFLNYLSLSDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTGM
40  AYDRYVAICKPLHYTIIMSRQKCNTIIVCCTGGFIHSASQFLTIFVPFCGPNEIDHYFCDVYPLL
    KLACSNIHMIGLLVIANSGLIALVTFVVLLLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF
    APALFIYIRPVTTFSEDKVFALFYTIIAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNQLF
    (SEQ ID NO: 103)


45  ATGTCATTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
    GCACTTTGTTTATTCTCTTGGGGTTTCCCAAAATAAGAACATTGAAGTCCTCTGCTTTGTA
    TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAAACTTACTCATAATGATTTCTATCAC
    GTGCACCCAGCTCATTCACCAACCCATGTATTTCTTCCTCAATTACCTCTCACTCTCCGACC
    TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
50  CATTTCCTATAATAACTGTATGATACAACTCTTTACCACCCATTTTTTGGAGGCATAGAGA
    TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCTGCACTA
    CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTTGTACTGGGGGA
    TTTATACATTCTGCCAGTCAGTTTCTTCTCCACCATCTTTGTACCATTTTGTGGCCCAAATGA
    GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
55  TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
    TTGTTGTCTTATGTGTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA
```

```
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTTGCTCCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGCCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTGGTGTTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
ID NO: 104)
```

AOLFR58 sequences:

```
MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPNVQEIVFVVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCDLYPLLELACTDTHIFGLMVVINSG
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)
```

```
ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCCTCCTGGGACTTTCACAGAATCCAAATGTTCAGGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAAACATGCTAATTGTAGTAACCATTCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCCTGTCCTTCCTGGA
TGCGTGCTTCTCATCTGTCATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCGTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCATTCCATGATACAAATTCTTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGCTTCCTTCTGTGTCATCTTGCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGGATTTTGTTCTTTGTCCCATGCA
TATTTGTATATACACGACCTCCATCTGCTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)
```

AOLFR59 sequences:

```
MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTILSVIWIESSLHQPMYYFI
SILAVNDLGMSLSTLPTMLAVLWLDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLPTPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSIYGLCVVIATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLIFFVPVIGVS
MVHRFGKHLSPIVHILMADIYLLLPPVLNPIVYSVRTKQIRLGILHKFVLRRRF (SEQ ID NO:
107)
```

```
ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCCTG
GACTGGAGTATGTTCATTCTTGGCTCTCCATCCTCTTCTGTCTTGCATATTGGTAGCATTT
ATGGGTAATGTTACCATCCTGTCTGTCATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA
TGCTTGCTGTGTTATGGTTGGATGCTCCAGGAAGTCCAGGCAAGTGCTTGCTATGGCTCAGCT
GTTCTTCATCCACACATTCACATTCCTGGAGTCCTCAGTGTTGCTGGCCATGGCCTTTGACC
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCCACATCCTCACCAACAGTGTAATTGGC
AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT
GAGACACTATCACTACTGCCATGGCACTACCTCTCACGCCCTTCTGTTTTGCACCAGGAT
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTGTGGATTCAACATCTTCATACTTCTTTCTTTATGTTCTGATTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCATA
TCTGTGTGGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTTCCCCCAGT
```

CCTTAACCCTATTGTCTATAGTGTCAGAACAAAGCAGATTCGTCTAGGAATTCTCCACAAG
TTTGTCCTAAGGAGGAGGTTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5
MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCAVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAVLVAMAYDSYVAICN
PLQYSAILTNKVVSVIGLGVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGLAHLSCASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVFRLPTHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF

10
(SEQ ID NO: 109)

ATGTTCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
ATAGGGAACTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT

15
TCTACTTCCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACTTCACACTTATGGAGTCAGCAGTTCCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTAATTTTCGTCATTCCCTCTATACTTC

20
TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
TTTGTAATCTGGTGTTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTTCCGTCTTCCTACTCATGAGCCCCGACTCAAGTCCCTCAAGCACGTGGTTCCACATGT
GTGTGTAATCCTTGCCTTCTATACACCAGCCCTCTTTTCCTTTATGACTCATTGCTTTGGCC

25
GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

30 **AOLFR61 sequences:**

MSIINTSYVEITTFFLVGMPGLEYAHIWISIPICSMYLIAILGNGTILFIIKTEPSLHGPMYYFLSML
AMSDLGLSLSSLPTVLSIFLFNAPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY

35
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPIINLAVVHRFAG
HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT

40
CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT
ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTTAAGCATCTTCCTGTTCAATGCCCCTGAAACTTCTTCTTCAGTGCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
GATTCCTAGCCATCCACAATCCTCCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC

45
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
TAAGAAGCTTGAAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAACGACTGT
ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC

50
TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
GCATGTCTCTCCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
TGAAACCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55
MFYHNKSIFHPVTFFLIGIPGLEDFHMWISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC

APLHYATILTSLVLVGISMCIVIRPVLLTLPMVYLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI
NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLPSHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
HRFGHQIPGYIHILVANLYLIIPPSLNPIIYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5
ATGTTTTATCACAACAAGAGCATATTTCACCCAGTCACATTTTTCCTCATTGGAATCCCAGG
TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC
TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGGCCCATGTT
CTACTTCCTGGCCATTCTTTCCACTATTGATTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
TGCTGGGTATCTTCTGGTTTGATGCTCACGAGATTAACTATGGAGCTTGTGTGGCCCAGAT
10
GTTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTTGGT
GGGCATTAGCATGTGCATTGTAATTGTCCCGTTTACTTACACTTCCCATGGTCTATCTTA
TCTACCGCCTACCCTTTGTCAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
CATTGCAAAATTGTCCTGTGGAAACATTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
15
CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
TTCCGGCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTTCCTTACTCATCGGATTGGACAC
CAAATACCAGGTTACATTCACATTCGTTGCCAATCTCTATTTGATTATCCCACCCTCTCT
CAACCCCATCATTTATGGGGTGAGGACCAAACAGATTCGAGAGCGAGTGCTCTATGTTTTT
20
ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFFLVGMPGLEYAHIWISIPICSMYLIAILGNGTILFIIKTEPSLHEPMYYFLSML
AMSDLGLSLSSLPTVLSIFLFNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS
25
ILTTVRVAQIGIVFSFKSMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLAVVHRFAR
HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
30
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTTAAGCATCTTCCTGTTCAATGCTCCTGAAATTTCATCCAATGCCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
35
GATTCCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
TAAGAAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
40
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
TGTGCAGTGATCATCTTCTACCTGCCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
GCATGTCTCTCCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
45
GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVILGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
50
HDSTVLTPACIVKMGLSSVLRSALLILPLPFLLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN
HIYGLFVVACTVGVDSLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
HRFGEHLPRVVHLFMSYVYLLVPPLMNPIIYSIKTKQIRQRIIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCCTGACGGGCTTCCAAG
55
GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
TTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT

-109-

```
        ACTATTTCTTGGGCATGCTAGCTGTCACAGACTTAGGCCTTTGCCTTTCCACACTGCCCACT
        GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
        TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
        CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG
    5   TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCCTC
        CTGAAGCGCTTCCAATACTGCCACTCCCATGTCTGGCTCATGCTTATTGTCTTCACCTGGA
        GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTGTTGTG
        GCCTGCACCGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC
        CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
   10   ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
        TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCTATGTGTATCTGCTGGTACCACCCC
        TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
        GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGGAAGGATTAA (SEQ ID NO: 118)
```

AOLFR65 sequences:

```
        MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFFVYLVALLGNTALLFVIQTEQSLHEPM
        YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFFTAMESIVLVAMAFDRYI
        AICKPLRYTMILTSKIISLIAGIAVLRSLYMVVPLVFLLLRLPFCGHRIIPHTYCEHMGIARLACAS
        IKVNIRFGLGNISLLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
   20   THRFGHNIPQYIHIILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)
```

```
        ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCTACTGCT
        GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT
   25   CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTTTGTGATCCAGACTGAGCAGAGTCTCC
        ATGAGCCTATGTACTACTTCCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
        CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC
        TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
        CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA
   30   GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCCTGAGGAGCCTGTACATGGTTGTTCC
        ACTGGTGTTTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
        GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
        CCTTGGCAACATATCTCTCTTGTTACTGGATGTTATCCTTATTATTTCTCTCCTCATGTCAGGA
        TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
   35   GGTTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTCATTCTTGACACA
        TCGTTTTGGCCATAATAATCCCACAGTATATACATATTTATATTAGCCAACCTGTATGTGGTTG
        TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTCGAGAGAGAG
        TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)
```

AOLFR66 sequences:

```
   40   MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
        ALLSFTDVLMCTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMLMALDHCVAI
        CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
        VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
        TFFTHHFGGHTIPLHIHIIMANLYLLMPPTMNPIVYGVKTRQVRESVIRFFLKGKDNSHNF (SEQ
   45   ID NO: 121)
```

```
        ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG
        GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
        ACAGGGAACTTCGGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
   50   ATGTCTTCCTTGCCCTTCTTTCCTTCACAGATGTGCTCATGTGCACCAGCACCCTTCCCAAC
        ACTCTCTTCATATTGTGGTTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
        GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
        CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
        TAAAGCTGGGTTCCTCACTTTTCTTAGGGGTGTGATGCTTGTTATCCCTTCCACTTTCCTCA
   55   CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCCACACCTACTGTGACCACATGTC
        TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
```

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCGACCGCTGCACTGCCCAC
TTCTGTGCCACTAGTCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
GGGACACACCATTCCTCTACACATACATATTTATTATGGCTAATCTCTACCTACTAATGCCTC
5   CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCATTA
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVVGNCGLICLISHEEALHRPMYYFLA
10   LLSFTDVTLCTTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVLMLMALDRYVAI
CYPLRYATILTNPVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVFDICCISVSYTMILQAVMSLSSADARHKAFSTCTSHMCCSIVITYVAAF
FTFFTHRFVGHNIPNHIHIIVANLYLLLPPTMNPIVYGVKTKQIQEGVIKFLLGDKVSFTYDK
(SEQ ID NO: 123)

15

ATGTCTGGGGACAACAGCTCCAGCCTGACCCCCAGGATTCTTTATCTTGAATGGCGTTCCTG
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
GTGGGGAACTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
20   ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTCACCCTTTGTGCACCACATGGTACCTAAT
ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCACTCTCCTC
25   ACCAAGGCGCTGCCCTATTGCCGGGGGAACTTCATCCCCCACACCTACTGTGACCATATGT
CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT
30   AGGACACAATATCCCAAACCACATACACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTCAGGAAGGTGTAATTA
AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTIWLEASLHQPL
35   YYLLSLLSLLDIVLCLTVIPKVLTIFWFDLRPISFPACFLQMYIMNCFLAMESCTFMVMAYDRY
VAICHPLRYPSIITDHFVVKAAMFILTRNVLMTLPIPILSAQLRYCGRNVIENCICANMSVSRLSC
DDVTINHLYQFAGGWTLLGSDLILIFLSYTFILRAVLRLKAEGAVAKALSTCGSHFMLILFFSTIL
LVFVLTHVAKKKVSPDVPVLLNVLHHVIPAALNPIIYGVRTQEIKQGMQRLLKKGC (SEQ ID
NO: 125)

40

ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTGCCCTGCGTGTCTGGGCTCCTTTTCCTCTTG
GCCGTAGGGGGCCAACACCCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGCACATCGTGCTCTGCCTCACTGTCATC
45   CCCAAGGTCCTGACCATCTTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCT
CCAGATGTACATCATGAATTGTTTCCTAGCCATGGAGTCTTGCACATTCATGGTCATGGCC
TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAACTCATCACTGACACTT
TGTAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
ATCCTTTCAGCACAACTCCGTTATTGTGGAGAAGTGTCATTGAAGAACTGCATCTGTGCCA
50   ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCAACCTTTACCAATTTGCT
GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCCTCTCCTACACCTTCATTCT
GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
CTCCCACTTCATGCTCATCCTCTTCTTCAGCACCATCCTCCTGGTTTTTGTCCTCACACATGT
GGCTAAGAAGAAAGTCTCCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
55   CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATG
CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFVLDFNMKNVTEVTLFVLKGFTDNLELQ
TIFFFLFLAIYLFTLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
5   KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMPLINASYVAGI
LHATIHTVATFSLSFCGANEIRRVFCDIPPLLAISYSDTHTNQLLLFYFVGSIELVTILIVLISYGLIL
LAILKMYSAEGRRKVFSTCGAHLTGVSIYYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV
IYSLRNKDVKDSMKKMFGKNQVINKVYFHTKK (SEQ ID NO: 127)

10   ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTTGTTCATT
CTTTTTGTCATAATATGAACTGTAACTTTATGCATATCTTCAAGTTTGTTCTAGATTTCAAC
ATGAAGAATGTCACTGAAGTTACCTTATTTGTACTGAAGGGCTTCACAGACAATCTTGAAC
TGCAGACTATCTTCTTCTTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA
15   GTATGTTGTCTTCTGTGGATGCCTGCTATTCCTCAGTTATTACCCCAAATATGTTAGTAGAT
TTTACGACAAAGAATAAAGTCATTTCATTCCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
GTAGTTTTGGAACCACAGAATGCTTCTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
CATCTACAACCCTCTCCTGTATTCAGTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
AATGCTTCCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
20   ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGTGATATCCCTCCTCTCCTTGCTA
TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTGATTCTGTTGGCCATTCTGAAGAT
GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCCAGCTATGCTTCG
25   GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAAATGTTTGGGAAAAATCA
GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

30   MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLLFFAI
YLFTLIGNLGLVVLVIEDSWLHNPMYYFLSVLSFLDACYSTVVTPKMLVNFLAKNKSISFIGCA
TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASYVAGILHATIHIVA
TFSLSFCGSNEIRHVFCDMPPLLAISCSDTHTNQLLLFYFVGSIEIVTILIVLISCDFILLSILKMHSA
KGRQKAFSTCGSHLTGVTIYHGTILVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
35   KAVKKMLKLVYK (SEQ ID NO: 129)

ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA
AGTTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
40   TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCCTATTTTTACTATTT
TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG
ATTCCTGGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCCTGGCAAAAAATAAATCCATTT
CATTTATCGGATGTGCAACACAGATGCTTCTTTTTGTTACTTTTGGAACTACAGAATGTTTT
45   CTCTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCTCTCCTGTATTCAGT
GAGCATGTCACCCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTTTAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG
GCATGTCTTTTGTGATATGCCTCCTCTCCTGCTATTTCTTGTTCTGACACTCACACAAACC
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTGCACTATCCTGATTGTGCCTCATT
50   TCCTGTGATTTCATTCTGTTGTCCATTCTGAAGATGCTTCTGCTAAGGGAAGGCAAAAGG
CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
AGTTATATGAGACCAAGTTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

MGRRNNTNVPDFILTGLSDSEEVQMALFILFLLIYLITMLGNVGMILIIRLDLQLHTPMYFFLTH
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFFVFLGAAECFLLSSMAYDRYVAICSPLRY
PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI

5   MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLKPRK
SYSLGRDQVASVFYTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC

10   AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
TCCTTACTCACTTGTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
GCGAACTTACTGACTTCCAACTATATTTCCTTCATGGGCTGCTTTGCCCAGATGTTCTTTTT
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTATCTGCAGTCCTCTCACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC

15   ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTTCTGCGACACGTCTCCAATTTTAGCT
CTGTCCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCTGAAA
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG

20   TCACCATCTTTTATGGAACTATGATTTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
GGAAGGGATCAAGTGGCTTCTGTTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

25   **AOLFR72 sequences:**

MAPENFTRVTEFILTGVSSCPELQIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTTSFYBECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVVSRRLCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFYCDNVPLLALSCSDTYLPE
TVVFISAATNVVGSLIIVLVSYFNIVLSILKICSSEGRKKAFSTCASHMMAVTIFYGTLLFMYVQP

30   RSNHSLDTDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:
133)

ATGGCTCCTGAAAATTTCACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCCCTCTTCCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG

35   GAACCTGGGCATCATCACCCTCACCAGTGTTGACTCTCGACTTCAAACCCCCATGTACTTTT
TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCATTGCCCCTAAAATGCTG
ATTAACTTTTTAGTAAAGAAGAAAACTACCTCATTCTATGAAGTGCCACCCAACTGGGAG
GGTTCTTGTTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
GTGGCTATTTGTAACCCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT

40   GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
CTGTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCCTCTGTTA
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA
ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
AAAATATGTTCATCAGAAGGAAGGAAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG

45   CAGTCACAATTTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTTACACGTTGGTAATTCCTATGCTGAAT
CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
AATCTGTGCTATTCCTTTAAAACAATGTAA (SEQ ID NO: 134)

50   **AOLFR73 sequences:**

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFGLFLIIYLVTVIGNLGMVILTYLDSKLHTP
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISELFILSAMAYDRYV
AICKPLLYVIIMAEKVLWVLVIVPYLYSTFVSLFLTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
NELELIILIFSGCNLLFSLSIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL

55   QPKSSHTLAIDKMASVFYTLLIPMLNPLIYSLRNKEVKDALKRTLTNRFKIPI (SEQ ID NO: 135)

-113-

```
ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
CACACCCCCATGTACTTTTTCCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
CATTGCCCCGAAGATGTTAGTAAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
AATGGCCTATGATCGCTCACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
TCTCACAATTAAGTTATTTAAACTGTCCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTTATTATTTACTTGCA
ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA
AGAGAACTTTAACCAATCGATTCAAAATTCCCATTTAA (SEQ ID NO: 136)
```

AOLFR74 sequences:

```
MEQHNLTTVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
LAFMDLGYSTTVGPKMLVNFVVDKNIISYYFCATQLAFFLVFIGSELFILSAMSYDLVVAICNPL
LYTVIMSRRVCQVLVAIPYLYCTFISLLVTIKIFTLSFCGYNVISHFYCDSLPLLPLLCSNTHEIELI
ILIFAAIDLISSLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)
```

```
ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCTCATGATCTATGTGATCTCAGTGATGG
GCAATTTGGGCATGATTGTCCTCACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTTT
TTTCTCAGACATCTGGCTTTCATGGATCTTGGTTATTCAACAACTGTGGGACCCAAAATG
TTAGTAAATTTTGTTGTGGATAAGAATATAATTTCTTATTATTTTTGTGCAACACAGCTAGC
TTTCTTTCTTGTGTTCATTGGTAGTGAACTTTTTATTCTCTCAGCCATGTCCTACGACCTCT
ATGTGGCCATCTGTAACCCTCTGCTATACACAGTAATCATGTCACGAAGGGTATGTCAGGT
GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTTCTTCTTCTAGTCACCATAAAGATTT
TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
TGATTTGATTTCATCTCTTCTGATAGTTCTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG
GTCATAGTGTTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCTT
TGACACTGATAAAGTGGCTTCCATATTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA
TCTATAGTTTACGAAACAAAGATGTAAAATATGCCCTACGAAGGACATGGAATAACTTATG
TAATATTTTTGTTTAA (SEQ ID NO: 138)
```

AOLFR75 sequences:

```
MEGKNQTNISEFLLLGFSSWQQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA
NLSLVDLCLPSATVPKMLLNIQTQTQTISYPGCLAQMYFCMMFANMDNFLLTVMAYDRYVAI
CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMAHLHFCSDNVIHHFFCDINSLLPLSCSD
TSLNQLSVLATVGLIFVVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFIYSLRNNELKGTLKKTLSRPGAVAHACNPSTL
GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)
```

```
ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
AACAACAGCAGGTGCTACTCTTTGCACTTTTCCTGTGTCTCTATTTAACAGGGCTGTTTGGA
AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
CCTTGCCAATCTGTCCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCTGGCTGCCTGGCTCAGATGTATTT
CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC
GTGGCCATCTGTCACCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT
```

```
GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC
ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC
CCTCTGTCCTGTTCCGACACCAGTCTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
5    AAAGTCCCTTCTGCCCAAGGAAAACTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT
ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGGTTGTAGCACCTGTGTTGAATCCAT
TCATTTACAGTTTAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
10   TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)
```

AOLFR76 sequences:

```
MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMIILILLDSHLHTPMYFFLSNLSLA
GIGYSSAVTPKVLTGLLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
15   TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIHHFFCDKPAVITLTCSEKHISELIL
VLISSFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLFYITVIIMYIRPSSSHSM
DTDKIASVFYTMIIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)
```

```
ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
20   CTACAGGTTCCCCTTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA
GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG
GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTTGT
25   GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCCTCAATGGCCTATGACCGGCTACGCAG
CAGTGTGTAACCCCCTACATTATACCACCACCATGACAACAACGTGTGTGGTCTTGTCTGGC
TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTCGCC
TCTCTTTCTGCATGTCCAATGTGATTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
TGCAACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCCATTGCCATT
30   TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTTCCAGTCATTCCATGGA
CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
ATTCTCTAGATTCAGTCTTTTAA (SEQ ID NO: 142)
```

35

AOLFR77 sequences:

```
MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVLMSYDRYVAVC
40   QPLQYPVLMRRQVCLLMMGSSWVVGVLNASIQTSITLHFPYCASRIVDHFFCEVPALLKLSCA
DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGLFYGA
AVFMYMVPCAYHSPQQDNVVSLFYSLVTPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)
```

```
ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
45   CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGTCATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
TCCTCACACTGATGGGTGTGGCTGAGGGCGTCCTGTTGGTCCTCATGTCTTATGACCGTTA
50   TGTTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC
TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCTTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGGCCACGTGTTGCAGGCTGTT
55   CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCACCACCTGCTCCTCGCACATCA
CGGTAGTGGGGCTCTTTTATGGTGCCGCCGTGTTCATGTACATGGTGCCTTGCGCCTACCA
```

CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5　　**AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLLVYLLNLTGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLLAVMSADRYLAICH
PLRYPLLMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLLRLAC
TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
10　　FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFIYALRNEQVKEALKDMFRKVVAGVLGNLLLD
KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTTGTCTATCTCCTGAATCT
15　　GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTCATCATTCCAA
AGATGCTGAGCAATTTCCTCTCAAGGCAACACACTATTTCCTTTGCTGCATGTATCCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCCTCCGAGTTCTTACTGTTGGCTGTCATGTCTGCGG
ATCGCTACCTGGCCATCTGTCATCCTCTGCGGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
20　　CTTTCGTGTGGCCTTGCTTCCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCCTGGCTTGCACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTGCTCATTGTATCTTCCTTGCTGATCACTGCTGTTGTCCTACGGCCTCATTG
TGCTGGCAGTCCTGAGCATCCCCTCTGCTTCAGGCCGTCAGAAGGCCTTCTCTACCTGTAC
25　　CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC
CACTGTTGAATCCATTCATCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

30

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMALIFTDSHLQSP
MYFFLNVLSFLDICYSSVVTPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAYDR
FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSAIQTGNVFALPFCGPNQLTHYYCDIPPLLH
35　　LACANTATARVVLYVFSALVTLLPAAVILTSYCLVLVAIGRMRSVAGRBKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSVFYTIIIPMLNPFIYSLRNKEVKGALQRKLQVNIFPG
(SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCCAGTCACCAAGTTCATCT
40　　TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGGAGCCATCCTGCTCAT
CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
CTCCAAAGCCCAATGTATTTCTTCCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
GTGGTCACACCTAAGCTCTTGGTCAACTTCCTTGGTCTCTGACAAGTCCATCTCTTTTGAGG
GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCCTGCTGGC
45　　CTCCATGGCCTATGACCGCTTCCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCCTATGCATTTGGTGGAGCCAACTCCGC
TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCAACATTCAACACACTAC
TACTGTGACATACCACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
TCCTCTATGTCTTTTCTGCTCTGGTCACCCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
50　　GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT
GTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

55

AOLFR80 sequences:

MEGINKTAKMQFFFRPFSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFFVFLGGADCVLLVVMAYDRFIAICH
PLRYRLIMSWSLCVELLVGSLVLGFLLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR
5   VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVVLLQYGCTSFIYLSPS
SSYSPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

      ATGGAAGGAATAAATAAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC
      CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGTATCTGACCAGCCTCGGTGG
10   AAATGCTACAATTGCAGTCATTGTTCAGATCAATCATTCCCTCCACACCCCCATGTACTTTT
      TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTGGCCTTG
      GCAAACCTCCTTTCAATGGGCAAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
      TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCCTGCTGGTAGTCATGGCTTATGACCGG
15   TTTATAGCGATCTGTCACCCTCTGCGATACAGGCTCATCATGAGCTGGTCCTTGTGTGTGG
      AGCTGCTGGTAGGTCCTTGGTGCTGGGGTTCCTGTTGTCACTGCCACTCACCATTTTAATC
      TTCCATCTCCCATTCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
      CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
      ATCGTCCTTAGCCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
20   TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
      TTAGTGGTCCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCCAGCTA
      CTCTCCTGAGATGGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
      CCCTTGATCTATAGTTTGAGGAACAAGGAACTGAAAGATGCCCTAAGGAAAGCATTGAGA
      AAATTCTAG (SEQ ID NO: 150)

25   **AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAELQLPLFCLFLGIYTVTVVGNLSMISIIRLNRQLHTPMYYFLSS
LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSPRMMSNQTLVTEFILQGFSEHPEYRVFLFSCF
LFLYSGALTGNVLITLAITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
30   MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCSGLATAVWLLCAVNTAIH
      TGLMLRLDFCGPNVIHHFFCEVPPLLLLSCSSTYVNGVMIVLADAFYGIVNFLMTIASYGFIVSSI
      LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
      IYTLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

      ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
35   ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
      ACCGGGTGTTCTTATTCAGCTGTTTCCTCTTCCTCTACTCTGGGGCCCTCACAGGTAATGTC
      CTCATCACCTTGGCCATCACGTTCAACCCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT
      CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT
40   CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
      CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC
      ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
      TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
45   CTCTCCTGCAGCTCCACCTACGTCAACGGTGTCATGATTGTCCTGGCGGATGCTTTCTACG
      GCATAGTGAACTTCCTGATGACCATCGCGTCCTATGGCTTCATCGTCTCCAGCATCCTGAA
      GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG
      GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
50   CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACCTGTGCTGAGTCCTACCCTCAACCCCCT
      CATCTATACTTTGAGGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC
      AGAAATTAA (SEQ ID NO: 152)

      AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIIISVKASQALKNPMFFFLFYLSL
55   SDTCLSTSIAPRMIVDALLKKTTISFSECMIQVFSSHVFGCLEIFILILTAVDRYVDICKPLHYMTII
      SQWVCGVLMAVAWVGSCVHSLVQIFLALSLPFCGPNVINHCFCDLQPLLKQACSETYVVNLLL

-117-

VSNSGAICAVSYVMLIFSYVIFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
5   GGAAGAAAATAGTGTTTGTTATTTTTTTGCGTCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCCTT
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCTCATCCTCACGGCTGTTGACCGCTATGTGGA
10   CATCTGTAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTTTTGATG
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTTGAAA
CAAGCCTGTTCAGAAACCTATGTGGTTAACCTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTCATGCTAATATTCTCCTATGTCATCTTCTTGCATTCTCTGAGAAAC
15   CACAGTGCTGAAGTGATAAAGAAAGCACTTTCCACATGTGTCTCCCACATCATTGTGGTCA
TCTTGTTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT
AAGATGATAGCTGTATTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)
20

AOLFR83 sequences:

MGNWTAAVTEFVLLGFSLSREVELLLLVLLLPTFLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMSYDRYATICCPLRYT
TIMRPSVCIGTVVFSWVGGFLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
25   MLSSMVILCCIVLVAYSYTYIILTIVRIPSASGRKKAFNTCASHLTIVIIPSGITVFIYVTPSQKEYL
EINKIPLVLSSVVTPFLNPFIYTLRNDTVQGVLRDVWVRVRGVFEKRMRAVLRSRLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTTCTGCTGGGGTTTTCCCTGAGCAGGG
30   AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCCACGTTCCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGTCCTGCTCCGCCTCCACACCCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTCACCTCAGTCATCTCTCCAAAAGTGTTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCTTTTGCCGGATGTATCACCCAGTGCTATTTCT
35   ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
TTGTATTCTCTTGGGTGGGAGGCTTCCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCCAG
CTGCCCTTCTGTGGCTGCAATATCATTAACCACTTCTTCTGTGACAGTGGACCCTTGCTGGC
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
40   ATCCTCTGCTGCATAGTCCTCGTGGCCTATTCCTATACGTACATCATCTTGACCATAGTGCG
CATTCCTTCTGCAAGTGGAAGGAAGAAGGCCCTTTAATACCTGTGCTTCCCACCTGACCATA
GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCCTCAACCCCTTT
ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT
45   CGAGGAGTTTTTGAAAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

MGAKNNVTEFVLFGLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
50   SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILIISYVIILLNLRSQSSEDRRKAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIILFNIVMPPLLNPLIYTLRNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55   ATGGGTGCCAAGAACAATGTGACTGAGTTTGTTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT

```
CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATACCCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
```
5
```
CTTCTTTGGTGGCACTGAGATCTTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCGTCGCAGACCCTCCTCACGGTTCAGCTG
CCTTTTTGTGGGCCCAATGAGATAGACAACTTCTTCTGTGATGTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
```
10
```
TTAGCATCCTTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCCTT
TTGGTTCTCATGCCCCCCATGTTCATGTACATTCGTCCCTCCACCACCCTGGCTGCTGCACAA
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)
```
15

AOLFR86 sequences:
```
MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFQAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC
```
20
```
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)
```

25
```
ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTTGCTGATCTATGTGG
TCACGGTTTGTGGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGTATTTTTTCCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
```
30
```
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCCTGCATTCATTGGTTCAG
CTCCTCCTGGTCCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
```
35
```
CTTGTACCCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTTAATCTGCCTGTTGAACTTCCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCCTTGTTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
```
40
```
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)
```

AOLFR87 sequences:
```
MNNIAQLSLGFIDLGIPSVLQKIILTKIILLFKMYVSNCNPCAIHRKINYPNTKLDFEQVNNITEFI
LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIIVVTITTSPALDSPVYFFLSFFSFIDGCSSSTMAP
KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYYLITMNRQVCGL
```
45
```
LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCIDTHVFGLFVAANSGLM
CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFFVPCILVYLRPMTFPIDKAVSVFYTVVTPM
LNPLIYTLRNTEVKNAMKQLWSQIIWGNNLCD (SEQ ID NO: 161)
```

50
```
ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
TTGTGCTATTCACAGAAAAATCAATTATCCAAATACCAAACTGGATTCGAGCAAGTGAAC
AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGGCAGAGGCACAGAAACTCTTGT
TTGCTGTGTTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
```
55
```
ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGTATTTTTTCTGTCTTTCTTTTCCTTCAT
AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG
```

```
        AAAACTATTTCCTTCAGTGGGTGCATGACCCAGCTCTTGTAGAACATTTCTTTGGGGGAG
        TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT
        GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
        GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
   5    CAATGTCATTGACCATTTCATCTGTGACCTTTTCCCTCTGCTAAAACTCTCCTGCACTGACA
        CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
        ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTCTACCTGCGC
        CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
        TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
   10   AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
        AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)
```

AOLFR88 sequences:

```
        MWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
   15   LSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLLAVMSYDRYVAICH
        PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFPAVVKLVC
        GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
        YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRRDVITQCIQRLQLWLP
        RV (SEQ ID NO: 163)
   20
        ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
        CCCTTACCCACCTTTTCCTTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
        AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCCAATGTATTTCCT
   25   GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
        ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
        TCTATTTGTGTCTAGGTGGTGCTGAATGTTTTCTCTTAGCTGTCATGTCCTATGACCGCTAT
        GTTGCCATCTGTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
        TGGCTGTCATGTCATGGTTGGGGGGCATCGGTGAACTCCCTAATTCACATGGCGATCTTGAT
   30   TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
        CCTCCTCCTCCCCATCTTCCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCATTCA
        GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCATGAAGCAGCTGTGGCTCCACCTCACGGTG
        GTTTCTCTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCACTCT
        ATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCACATTGAATTCTCTG
   35   ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
        GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
        164)
```

AOLFR89 sequences:

```
   40   MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVS
        GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYL
        CLGGAECFLLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF
        PFCGPRKVYHFYCEFPAVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
        RNAFATCGSHLTVVSLWFGACIFSYMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
   45   KALRRVLRRDVITQCIQRLQLWLPRV (SEQ ID NO: 165)
```

```
        ATGCTGGACCCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
        GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
        GCTCTTCGATGACTCCCTTACCCACCTTTTCCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
   50   TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
        CCAATGTATTTCCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
        CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
        ACCCAGCACTTCCTCTATTTGTGTCTAGGTGGTGCTGAATGTTTTCTCTTAGCTGTCATGTC
        CTATGACCGCTATGTTGCCATCTGTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
   55   GTGGGACTGATGATGGCTGTCATGTCATGGTTGGGGGGCATCGGTGAACTCCCTAATTCACA
        TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA
```

GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCCTGATTTCTACATCCTATGTCTTCATCCTT
CAAAGTGTCATTCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACCATGGACCCAGG

5   TCCCAGTGCACTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
TAG (SEQ ID NO: 166)

10   **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPNVQEIVFVVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL

15   CGILMGVAWTGGLLHSMIQILFTFQLPFCGPNVINHFMCDLYPLLELACTDTHIFGLMVVINSG
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA

20   TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTGTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCCTCCTGGGACTTTCACAGAATCCAAATGTTCAGGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCCTGTCCTTCCTGGA

25   TGCGTGCTTCTCATCTGTCATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCGTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCATTCCATGATACAAATTCTTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA

30   TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCATCTTGCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTTCTTTGTCCCATGCA
TATTTGTATATACACGACCTCCATCTGCTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT

35   ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

40   MGNWSTVTEITLIAFPALLEIRISLFVVLVVTYTLTATGNITIISLIWIDHRLQTPMYFFLSNLSFL
DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLGCWVGAFLSVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFLL
SALVILSSLAFITGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVAAVLITVVTPLLNPFIYSLRNEKVQEVLRETVNRIMTLIQRKT (SEQ ID NO: 169)

45   ATGGGAAACTGGAGCACTGTGACTGAAATCACCCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTTCTTCCTCA
GTAATTTGTCCTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGCTGGTTGCATGATCCAAACATATTTCTACT

50   TCTTTCTGGGGACGGTGGAGTTTATCCTCTTTGGCTGGTGATGTCCTTTGACCGCTACATGGC
TATCTGCGACCCACTGCACTACACAGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCCTGTCTGTGTTGTTTCCAACCATTGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCTCTTCTTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTCATCCT

55   GAGCTCCCTGGCATTCACTACTGGGTCCTACGTGTACATAATTTCTACCATCCTGCGTATCC
CCTCCACCCAGGGCCGTCAGAAAGCTTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC

-121-

ATTGCCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCACAGTGGTGACCCCTCTCCTGAACCCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGGAAAACTTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIIATVWAEPRLQIPMYFFLCNLSFLE
IWYTTTVIPKLLGTFVVARTVICMSCCLLQAFFHFFVGTTEFLILTIMSFDRYLTICNPLHHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMLLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
10   TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCTTGCAGGCAATGGG
15   CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATTCCAATGTACTTCTTCCTTTG
TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCTTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCTTCACCACCCCACCATCATGACCAGCAAACTCTGACCTGGCCC·
20   TGAGCTCCTGGGTGGTGGGCTTCACCATTGTCTTTTGTCAGACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGAAA
GCCGCCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTGA
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
25   CTCCCTGCTCTACGGGGCTGTTCTGTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG·
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

30   **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTTIVPVMLWGLLLPGMQITYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVVNNFFCDRGQLLKLSCN
NTLFTEFILFLMAVFVLFGSLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
35   VKPKQTQAADYNWVVSLMVSVVTPFLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTTGCTATATTCTTCTTTTTCTACTTGGTGACATTAATGGGAAACA
40   CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG
GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
TACCTTGCTGTGGGGCAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
·45   TGGCTGTCTGTAACCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
GGTTCTTGTGTCATGGGTGTTTGGGTTTCTTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTTTGTGACCGAGGGCAATTGCT
CAAACTATCCTGCAATAATACTCTTTTCACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
50   AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
TGTTGTGATTGGCTACGGCAGCTGCTTGTTTCTCTACGTGAAACCCAAGCAAACGCAGGCA
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACTCCTTTCCTCAATCCTTT
CATCTTCACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGTCAACTATTCAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFSVVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSLMDLMLVCTNVPKMAANFLSGRKSISFVGCGIQIGLFVCLVGSEGLLLGLMAYDRYVA
ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFFCEMLSLLKLAC
5   VDTSLFEKVIFACCVFMLLPPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
(SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCCTCTTAGGCATCTTCTCCC
10 ACAGTACTGCTGACCTTGTCCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
GGGAATGTCCTCCTCATCTTCCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT
CTTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
GCAGCCAACTTCCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG
GCCTCTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCGTCATGAATCAGAGGGTCTGTCTCC
AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG
TCTTCATGCTTCTCTTCCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
20 GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
TGACAGCTGTCACCCTCTTCTATGGGGCAGCCATGTTCATCTACCTGAGGCCTAGGCACTA
CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCCTTACTCCCATGCTC
AACCCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
GACCGGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)
25

AOLFR95 sequences:

MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
30 LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRLCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
RAVDHFYCDSRPLQRLSCSDLFIHRMISFSLSCIIILPTIIVIIVSYMYIVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
KKNIIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG
CTTCAGGGTACGCCCAGAGCTCCACATTCTCCTCTTCCTGCTATTTTTGTTTGTTTATGCCA
TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
ACCAATGTATTTTTTCCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCATCTGTTATTGA
ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
40 GCCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC
TTATGACCGCTTTATTGCCATCTGCAACCCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTCAGACT
AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC
TCGCCCACTTCAGAGACTGTCTTGTTCTGTATCTCTTTATCCATAGAATGATATCTTTTTCCT
45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGCTGTCTTTTTTATGTATCTCACTCCTGAC
AGATTTCCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAAAATTTCTAGA
50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN
LSLLEVCFTLVMVPKMLVDLVSPRKIISFVGCGTQMYFFFFGSSECFLLSMMAYDRFVAICNP
55 LHYSVIMNRSLCLWMAIGSWMSGVPVSMLQTAWMMALPFCGPNAVDHFFCDGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

-123-

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ ID NO: 179)

```
     ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
  5  CCGAGATGCAAGTTTCCCTCTTTATTTTTTTCCTGGCCATTTATACAGTCACTTTGTTGGGC
     AACTTTCTTATTGTCACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
     TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAAATGCTTG
     TAGATCTAGTGTCCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
     CTTCTTCTTCTTTGGCAGTTCTGAATGTTTCCTTCTCTCCATGATGGCTTATGATCGCTTTGT
 10  GGCCATCTGTAACCCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
     GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG
     CCCTTCCTTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
     AAACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
     TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCCTACACCCGCATTATCATAACAATTCTG
 15  AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
     GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAGTCC
     CCTGAGAGCAAGAAGCTAGTGTCATTGTCCTACACTGTCATCACACCTATGCTAAAACCCCA
     TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA
     AGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)
 20
```

AOLFR97 sequences:

```
     MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSFMVVPSFSIAEHWRRMKGANLSQGMEFEL
     LGLTTDPQLQRLLFVVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLLKSLSFLDFCYSSTVV
     PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
 25  ASLIVGSYSAGFLNSLIHTGCIFSLKFCGAHVVTHFFCDGPPILSLSCVDTSLCEILLFIFAGFNLLS
     CTLTILISYFLILNTILKMSSAQGRFKAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
     VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)
```

```
     ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
 30  CCTTAGGCAGAATTAAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
     TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
     GGAGTTTGAGCTCTTGGGCCTCACCACTGACCCCCAGCTCCAGAGGCTGCTCTTCGTGGTG
     TTCCTGGGCATGTACACAGCCACTCTTGCTGGGAACCTGGTCATGTTCCTTCTCATCCATGT
     TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
 35  TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACTTCTTGGCCAAGAGGGAAAGTGA
     TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAGTGAGTGC
     TATCTCATCGCTGCCATGGCCTATGACCGCTATTGTAACCCCCTGCTCTACTC
     AACCATCATGTCTCCTGAGGTCGTGCCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
     CTCAATTCTCTTATCCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCGT
 40  CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCCTTGTCTTGTGTAGACACCTCACTGT
     GTGAGATCCTGCTCTTCATTTTTGCTGGTTTCAACCTTTGAGCTGCACCCTCACCATCTTG
     ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCCACGGGCAGGTTTA
     AGGCATTTTCCACCTGTGCATCCCACCTCACTGCCATCGCTGCCTCTTCTTTTGGCACAACACTT
     TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCCAGGACCGCACAGTTGCTGTCA
 45  TCTACACAGTGGTGATCCCAGTGCTGAACCCCCTCATGTACTCCTTTGAGAAACAAGGATGT
     GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)
```

AOLFR98 sequences:

```
     MRGFNKTTVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLFI
 50  LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR
     YTLINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
     LALFSLSILVIMVPFLLILISYGFIVNTILKIPSAEGKKAFVTCASHLTVVFVHYGCASIIYLRPKSK
     SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)
```

```
 55  ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGGTTTCTCCAGCC
     TGGGGGAGCTCCAGCTGCTGCTTTTTGTCATCTTTCTTCTCCTATACTTGACAATCCTGGTG
```

```
GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
GCTTTCTATTCATCCTTTCATTTTCTGAGTCCTGCTACGCTTTTGTCATCATCCCTCAGCTGC
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
CTTTTTCCTTGGCTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGGATATGATCGCT
ATGTAGCAATTTGTCACCCTCTGAGGTACACACTCATCATAAACAAAAGGCTGGGGTTGGA
GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCACTATTTCTGTGACATGGCACCTGT
TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC
CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTCACCTGTGCCTCACATCTCACT
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAAACTGCATTGAAAAGAGTTCTTGGAATG
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)
```

AOLFR99 sequences:

```
MERVVNETVVREVIFLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC
SEICYTFIIVPKMLVDLLSLQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
LMGHGVCMGLVAAACACGFIVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV
IFMLCTLVLAIPLLLILVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)
```

```
ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTGTTATCTTCCTGCTCTCTACCTGTTCACTCTGGGCACC
AATGCAATCATCATTTCCACCATTGTCCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
CCTTGCCATCCTCTCTGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG
TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCCTGGGCTGTGCCATCCAAATGTTTTCC
TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA
CCTGCCTTTTTATTCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCCTCA
AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
CTGGCTATCCCCTTATTGTTGATCTTGGTGTCCTATGTTCACATCCTCTCTGCCCATACTTCA
GTTTCCTTCCACATCTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCCATTATTG
TCACTGTCCACTATGGCTGGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACTACTCCTCA
AGCCAGGAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
TTCCCTGTTGTAA (SEQ ID NO: 186)
```

AOLFR101 sequences:

```
MDTGNWSQVAEFIILGFPHLQGVQIYLFLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDFPPVLSLACTDTSINV
LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
KSYSLDYDQALAVVYSVLTPFLNPFIYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)
```

```
ATGGACACAGGGAACTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCCATCTCC
AGGGTGTCCAGATTTATCTCTTCCTCTTGTTGCTTCTCATTTACCTCATGACTGTGTTGGGA
AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
TTGTCAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
GCAAACTTGCTCAGTGAGAAAAAGACCATTTCATTCTCTGGGTGTCTCCTGCAGATCTATT
TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
TTTAGCCATCTGCCGGCCCCTCCACTACCCAAACCCTCATGACCCCAACACTTGTGCAGAG
ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCCTTGATTT
CACGCCTCCCATTCTGTGGCCCCAATCGCATTCAGCACGTCTTTTGTGACTTCCCTCCTGTG
CTGAGTTTGGCTTGCACTGATACGTCTATAAATGTCCTAGTAGATTTGTTTATAAATTCCTG
```

CAAGATCCTAGCCACCTTCCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
TCAGAATTCCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCTTCCTCACCT
5   CCTTCATCTACAGCTTGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

AOLFR102 sequences:

MPVGKLVFNQSEPTEFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIIWVVCTHSTLRTPMYF
10   FLSNLSFLELCYTTVVVPLMLSNILGAQKPISLAGCGAQMFFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVLRLACA
DIRVHQAVLYVVSILVLTIPFLLICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIIRKAASDAN (SEQ ID
NO: 189)

15

ATGCCTGTGGGGAAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT
TCACCACAGCCACTGAATTCCAGGTTCTTCTCTTCCTTCTCTTCCTCCTCCTCTACTTGATG
ATCCTCTGTGGCAACACAGCCATCATCTGGGTGGTGTGCACACACAGCACCCTCCGCACCC
CGATGTATTTCTTCCTGTCCAACCTGTCTTTCCTGGAACTCTGCTACACCACCGTGGTAGTA
20   CCCTTGATGCTTTCCAACATTTTGGGGGCCCAGAAGCCCATTTCGTTGGCTGGATGTGGGG
CCCAAATGTTCTTCTTTGTCACCCTCGGCAGCACGGACTGTTTCCTCTTGGCGATCATGGCC
TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCTCATCATGACCCGCGAGC
TGTGCACGCAGATGCTGGGTGGGGCCCTGGGCCTGGCCCTCTTCCCCTCCCTGCAGCTCAC
CGCCTTAATCTTCACCCTGCCCTTTTGCGGCCACCACCAGGAAATCAACCACTTCCTCTGCG
25   ATGTGCCTCCCGTCCTGCGCCTGGCCTGCGCTGACATCCGCGTGCACCAGGCTGTCCTCTA
TGTCGTGAGCATCCTCGTGCTGACCATCCCCTTCCTGCTCATCTGCGTCTCCTACGTGTTCA
TCACCTGTGCCATCCTGAGCATCCGTTCTGCCGAGGGCCGCCGGCGGGCCTTCTCCACCTG
CTCCTTCCACCTCACCGTGGTCCTGCTGCAGTATGGCTGCTGCAGCCTCGTGTACCTGCGTC
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTCAC
30   CCCCTTACTCAACCCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCCAACTGA (SEQ ID NO: 190)

AOLFR103 sequences:

MAEMNLTLVTEFLLIAFTEYPEWALPLFLLLLFMYLITVLGNLEMIILILMDHQLHAPMYFLLSH
35   LAFMDVCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
PLLYVTILTQQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTCGESYT
QEVLIIMFAIFVIPASMVVILVSYLFIIVAIMGIPAGSQAKTFSTCTSHLTAVSLFFGTLIFMYLRG
NSDQSSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

40   ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCCTCTTGTTATTATTTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCCT
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCCAGATGCTGG
CAGTGCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
45   GTTCACCTTCTTTGGTTCCATCGACTGCTACCTCTTTGGCCCTCATGGCCTATGACCGCTACT
TGGCTGTGTGCCAGCCCCTGCTTTATGTCACCATCCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGCGCCCTGGTGCGGACAGTCTCAGCCTTC
ACTCTCTCCTTCTGTGGAACCAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
50   GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCCTACCTGTTTATCATCGTGGCCATCAT
GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCACCTGCACCTCCCACCTCACTGCT
GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACTCAGATCAGTCTTC
GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTCATCCCCATGTTGAATCCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
55   AAGTTGTCCTAA (SEQ ID NO: 192)

-126-

AOLFR105 sequences:

MQGLNHTSVSEFILVGFSAFPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
RYNVLMSLRGCTCRVGCSWAGGLVMGMVVTVSAIFHLAFCGHKEIHHFFCHVPPLLKLACGDD
VLVVAKGVGLVCITALLGCFLLILLSYAFIVAAILKIPSAEGRNKAFSTCASHLTVVVVHYGFAS
VIYLKPKGPQSPEGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCFTKLFPQNC (SEQ ID
NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
CCACCTCCAGCTGATGCTCTTCCTGCTGTTCCTGCTGATGTACCTGTTCACGCTGCTGGGCA
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCCTGGCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTCACCCACTCCTTCCTGCTCACTGTCATGGGCTACGACCGCTACG
TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCCTCCTATGCCTTCATCGTGGCCGCCA
TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTCGTGCACTATGGCTTTGCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCTCACACCCTTCCTCA
GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
CACCAAACTCTTTCCACAGAACTGCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

METANYTKVTEFVLTGLSQTPEVQLVLFVIFLSFYLFILPGNILIICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIISFDGCIAQLFFLHFAGASEMFLLTVMAFDLYTAICRPLHYA
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCLIALLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVVLMFGPSIYIYARPFD
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTCATCCTACCAGGA
AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCCTGACCTCTCCTATGTATTTCCT
GTTGGCTAATCTGGCCTTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
GTGGCTCTCTCCTGGAGGGGGGGCTTCATTCATTCTATCATACAGGTGGCTCTCATTGTTC
GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
CCGGATTGCCTGTGCCAACACCTTCCCAGAGGATGTTAGTGATGATCTGTAGTAGTGGTCTG
ATCTCTGTGGTGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGTTCAA
GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATTA
TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA
TTTTGTGTAAAGAAGAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSGFILVGILNDSGSPELLCATITILYLLALISNGLLLLAITMEARLHMPMYLLLGQ
LSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGGAEDLLLAFMAYDRYVAICH
PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPFCRAQEIRHLLCEIPHLLKVACAD
TSRYELMVYVMGVTFLIPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA
ATFMYVLPSSFHSTRQDNIISVFYTIVTPALNLPIYSLRNKEVMRALRRVLGKYMLPAHSTL
(SEQ ID NO: 197)

-127-

```
     ATGGAGCTCTGGAACTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
     GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTTGGCCCTGATCAG
     CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC
  5  CTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAGGCCCT
     TGCGGACTTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTC
     CTGGCACTGACAATGGGTGGTGCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
     ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
     CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC
 10  ATGCACTATCCCTTCTGCAGGGCCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCCACACT
     TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
     GACCTTCCTGATTCCCTCTCTTGCTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG
     TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACCTGCTCTTCCCACCT
 15  GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCCAGTTCCTTCC
     ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAACAATTGTCACTCCAGCCCTGAA
     TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGG
     AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)
```

AOLFR108 sequences:

```
 20  MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIIYLLTVLGNQLIIILIFLD
     SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGCTECALLAV
     MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSFTFHLPYWGQNIINHYFCE
     PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMQSGEGRLKAFSTCGSHLI
 25  VVVLFYGSGIFTYMRPNSKTTKELDKMISVFYTAVTPMLNPIIYSLRNKDVKGALRKLVGRKC
     FSHRQ (SEQ ID NO: 199)
```

```
     ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
     ACCAAACCTTTGTGTCCAAGTTTATCTTCCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
     CCTGCTATTTATCCTTTTCCTCATCATTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 30  TCATTCTCATCTTCCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTTCTTAGAAATCTCT
     CCTTTGCAGATCTCCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTTGGTTCACTTCTTGGTA
     AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTTCTTCTTGGTTG
     GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA
     GCCCCTGTACTACTCTACCATCATGACGACAACGGGTGTGTCTCTGGCTGTCCTTCAGGTCCT
 35  GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG
     GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
     ATAGACACTTACAGCACCAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
     CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 40  GGGGAAGGGAGACTCAAGGCTTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCCTCTT
     CTATGGGTCAGGAATATTCACCTACATGCGACCAAACTCCAAGACTACAAAAGAACTGGA
     TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATAATTTATAGC
     TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAAACTAGTTGGGAGAAAGTGCTTCTCT
     CATAGGCAGTGA (SEQ ID NO: 200)
```

AOLFR109 sequences:

```
     MLRNGSIVTEFILVGFQQSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
     HLSLLDVCFTTTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY
     PLNYVPIISQKVCVRLVGTAWFFGLINGIPLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
     WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 50  PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
     201)
```

```
     ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA
     CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 55  AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
     TCTTCCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCACTACCATCCCACAGATG
```

```
       TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
       ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
       TATGTTGCTATCTGCTACCCACTTAACTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
       GGCTTGTGGGAACTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTC
  5    ATTCCGAGAGCCCTTCCGCAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
       GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
       TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC
       ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
       TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 10    CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
       ACCCCATCATTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
       GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)
```

AOLFR110 sequences:

```
 15    MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLIILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
       DASYSFIVAPRMLVDFLSEKKVISYRGCITQLFFLHFLGGGEGLLLVVMAFDRYIAICRPLHCST
       VMNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL
       LMVFNSGLMTLLCFLGLLASYAVILCHVRRAASEGKNKAMSTCTTRVIILLMFGPAIFIYMCPF
       RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
 20    203)
```

```
       ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
       AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
       AATTTTCTCATTATTTTCACCATAAGGTCAGACCCTGGGCTCACAGCCCCCCCTCTATTTATT
 25    TCTGGGCAACTTGGCCTTCCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTGG
       TGGACTTCCTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
       CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTTGTGATGGCCTTTGACCGCTAC
       ATCGCCATCTGCCGGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
       TGATGTTGGCTCTGTGGCTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCTCATCCTC
 30    CGCTTGCCTTTTTGTGGCCCAAACCAGCTGGCCAACTTCTTCTGTGATGTCCGACAGGTCA
       TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
       GATGACACTCCTGTGCTTTCTGGGGCTTCTGGGCTTCCTATGCAGTCATCCTCTGCCATGTTC
       GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCATTA
       TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTCAGGGCCTTACCA
 35    GCTGACAAGATGGTTTCTCTCTTTCACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
       TACCCTTCGCAACCAGGAAGTGAAAACTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
       TGTCAAGTGGATTTTATAATAAGAAACTGA (SEQ ID NO: 204)
```

AOLFR111 sequences:

```
 40    MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLLIYLCALM
       GNVLIIMTTTLDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSLIHNNSISFLGCVSQVFLLLSS
       ASAELLLLTVMSFDRYTAICHPLHYDVIMDRSTCVQRATVSWLYGGLIAVMHTAGTFSLSYCG
       SNMVHQFFCDIPQLLAISCSENLIREIALILINVVLDFCCFIVIIITYVHVFSTVKKIPSTEGQSKAY
       SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIIYSLRNKAIKVALGMLIKG
 45    KLTKK (SEQ ID NO: 205)
```

```
       ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
       TTTCCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 50    TGGGGTTTTCTAACCAATAAAAATATGTGCATTTTGCATTCGATTCTCTTCTTTGTTGATTTAT
       TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACTTTGGACCATCATCTCC
       ACACCCCCGTGTATTTCTTCTTGAAGAATCTCATTTTCTTTGGATCTCTGCCTTATTTCAGTC
       ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACTCCATTTCATTCCTTGGCTG
       TGTTTCCCAGGTCTTTTTGTTGCTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
       TGTCCTTTGACCGCTATACTGCTATATGTCACCCTCTGCACTATGATGTGTCATCATGGACAGG
 55    AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
       ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT
```

GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAATTGCACTCA
TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTTCTACACTATGCTGCCCCC
AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTTLSVFFPSWSCGIQLPLSLRCCLIFSVRRKPFLLQDASFRPTSS
TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFIILITFFFIMISYARIIGAVLKIKTASGRKK
AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLTLDRTLAIVYSVLTPMVNPIIYSLRNKEIIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAAGGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGCACACCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTCATGA (SEQ ID NO: 208)

AOLFR114 sequences:

MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTITGNLLIILAIRFNPHLQTPMYFFLSFLS
LTDICFTTSVVPKMLMNFLSEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDRYVAVCDPF
HYVTTMSHHHCVLLVAFSCSFPHLHSLLHTLLLNRLTFCDSNVIHHFLCDLSPVLKLSCSSIFVN
EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFIYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCCTCATCGTGTACCTGGTCACCATAAC
AGGGAACCTGCTCATCATCCTGGCCATTCGGCTTCAACCCCCATCTTCAGACCCCTATGTATT
TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
CTGATGAACTTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACAACAGATGT
ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCCAGTCATGGCCTTTGACCG
CTATGTGGCCGTCTGTGACCCTTTCCACTATGTCACCACCATGAGCCACCACCACTGTGTCC
TGCTGGTGGCCTTCTCCTGCTCATTTCCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCATTTCTCTGTGACCTCAGCCCTCGT
GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT
TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTGTCTATTTACAGCCCCCATCCACCTAC
GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTCATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5   MEGFYLRRSHELQGMGKPGRVNQTTVSDFLLLGLSEWPEEQPLLFGIFLGMYLVTMVGNLLII
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIIPTLNPFIYSLRNRDMKEALG

10   KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC

15   ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CCTGTCATTAACTGATGCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGGCACAGCTATATTTCCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT

20   GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCCAGAAAGCCATCCCTCATTTCTATTGTGACCTCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCCTCACT
GTTCCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCATCTC
ATCTCCTGGAGGGAGGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG

25   CTCTTCTATGGGTCTCTTATGGGTGTGTATTTACTTCCTCCATCAACTTACTCTACAGAGGAG
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTCCCACGCTAAACCCATTCATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCAGTGGAAAAACA
TTCTTTTTATGA (SEQ ID NO: 212)

30   **AOLFR116 sequences:**

MDEANHSVVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCILFLVISWIIGIIHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV

35   TANSGFISLASFLILISYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPFPTSHLD
KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCCTCTTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCGTCACCTCGTTTACAGTCCCCCATGTACTTCCT

40   GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
ATGACCTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAACTGAGATGGTGCTGCTCATAGCCATGGCTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCCTGGATTATAGGTATTATTCACTCAGTGATTCAGTTGGCTTTTGTTGTA

45   GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCCTCGATTTAT
CAAACTGGCTTGCATAGAGACCTACACATTGGGATTCATGGTTACTGCCAATAGTGGATTT
ATTTCTCTGGCTTCTTTTTTAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTCAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
TGGTTTTGGTCTTGGGCCATTAATCTTTTCTATATTTTCCATCATCACATCACATCTTG

50   ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55   MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGIILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215).

ATGAATAACACTATTGTATTTGTCATAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC
TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTCAGG
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
TGTACAAACAGGTTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
CTTGTTGTCTTTGTGGGATCTAACTTGATATTCACTGGGTTGGTCGTCATCTTTTCCTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
ACATGTGCTTCCCACCTGACCGCAGTCACCATTTCTATGGGACACTCTCTTACATGTATTT
GCAGTCTCATTCTAATAATTCCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

AOLFR118 sequences:

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIIWQNPSLQQ
PMYIFLGILCMVDMGLATTIIPKILAIFWFDAKVISLPECFAQIYAIHFFVGMESGILLCMAFDRY
VAICHPLRYPSIVTSSLILKATLFMVLRNGLFVTPVPVLAAQRDYCSKNEIEHCLCSNLGVTSLA
CDDRRPNSICQLVLAWLGMGSDLSLIILSYILILYSVLRLNSAEAAAKALSTCSSHLTLILFFYTIV
VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFALTKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTCACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA
CTACTGTATCCTCTACGCACTTGCTCGCAAACACCCTCATCCTCATCATCATCTGGCAGAACCC
TTCTTTACAGCAGCCCATGTATATTTTCCTTGGCATCCTCCTGTATGGTAGACATGGGTCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGATAGATATGTGGCTATCTGTCACCCTCTTCGCTATCCATCAATTG
TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTCATGGTGCTGAGAAATGGCTTATTTGTC
ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT
TTGCCAGTTGGTTCTGGCATGGCTTGGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGAAGCCAAGGCCC
TGAGCACTTGTAGTTCACATCTCACCCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
ACAACATCATCCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAACTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

AOLFR119 sequences:

MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTTLPNALCFWFSLKEINFNACLAQMFFVHGFTGVESGVLMLMALD
RYIAICYPLRYATTLTNPIIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNIISHTYCDHMSVVKL
SCASIKVNVIYGLMVALLIGVFDICCISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIIITYVPA

FFTFFAHRFGGHTIPPSLHIIVANLYLLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

```
    ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
5   TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
    ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
    CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
    CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACTTCA
    ATGCTTGCTTGGCCCAGATGTTCTTTGTTCATGGGTTCACAGGTGTGGAGTCTGGGGTGCT
10  CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
    TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCCTGAGGGGTGTATTGCTGAT
    GATTCCTTTCCCATTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCCATA
    CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
    CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTTTGACATTTGTTGTATATCTTTGTCTT
15  ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
    CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
    TCTTTGCCCACCGTTTTGGGGGACACACAATTCCCCCTTCTCTTCACATCATTGTGGCTAAT
    CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
    ACGCAAGAGTGTCATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)
20
```

AOLFR120 sequences:

MQPYTKNWTQVTEFVMMGFAGIHEAHLLFFILFLTMYLFTLVENLAIILVVGLDHRLRRPMYF
FLTHLSCLEIWYTSVTVPKMLAGFIGVDGGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTFCGPNVIDHFSCDASPLLALS
25 CSDVTWKETVDFLVSLAVLLASSMVIAVSYGNIVWTLLHIRSAAERWKAFSTCAAHLTVVSLF
YGTLFFMYVQTKVTSSINFNKVVSVFYSVVTPMLNPLIYSLRNKEVKGALGRVFSLNFWKGQ
(SEQ ID NO: 221)

```
    ATGCAACCATATACCAAAAACTGGACCCAGGTAACTGAATTTGTCATGATGGGCTTTGCTG
30  GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTCACCTTG
    GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
    ATTTCTTCCTGACACACTTGTCCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
    ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAAATATCTCTTATGCTGGTTGCCTAT
    CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTTCCTACTGGCTGCCATGGCC
35  TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC
    CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCCTCACACCCATCTTGCCAATCT
    ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTTCTCCTGTGATGCC
    TCACCCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGGAAGGAGACTGTGGATTTCCTGG
    TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGGTTCTGTCTATGGCAACATCGTC
40  TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
    CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
    GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTCACGCCCAT
    GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
    TTTTCTCTCAACTTTTGGAAGGGACAGTGA (SEQ ID NO: 222)
45
```

AOLFR121 sequences:

MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLTVYILTLVANIIIVTIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
50 TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPFCGTVVDHFFCDIYPVMKLSCIDTTINEII
NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLLNPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

```
    ATGAAGAGAAAGAACTTCACAGAAGTGTCAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
    GAAAGCATCAGATAACCCTCTTTGTGGTTTTCCTAACTGTCTACATTTTAACTCTGGTTGCT
55  AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
    CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT
```

```
      TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
      TTTTGTTATCTTGGCCACTAATAATTGCTTCCTGCTTACTGCAATGGGGTATGACCGCTATG
      TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCCAGCT
      GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTC
   5  AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA
      AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAAATTATGGTGTAAGTTCATTTGT
      GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTCATCTCTTCCATCCTTC
      AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCCACCTCACTGT
      GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
  10  ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCTG
      TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
      ATATTTCTTAA (SEQ ID NO: 224)
```

AOLFR122 sequences:

```
  15  MEWENQTILVEFFLKGHSVHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
      SFLDICYTTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
      YPIIMSKNAYVPMAVGSWFAGIVNSAVQTTFVVQLPFCRKNVINHFSCEILAVMKLACADISGN
      EFLMLVATILFTLMPLLLVISYSLIISSILKIHSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
      KETLNSDDLDATDKIISMFYGVMTPMMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
  20  225)
```

```
      ATGGAATGGGAAAACCAAACCATTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTCACC
      CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
      AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
  25  TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
      TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCTTTTCTGGCTGTGCAGTGCAGATGTTCCTT
      GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
      TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
      GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAAACTACATTTGTAGTA
  30  CAATTGCCTTTCTGCAGGAAGAAGTGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT
      GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
      TTCACATTGAGTGCCACTGCTCTTGATAGTTATCTCTTACTCATTAATAATTCCAGCATCCT
      CAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
  35  GTGGTCATAAATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
      CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
      GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
      AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)
```

AOLFR123 sequences:

```
  40  MYRFTDFDVSNISIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLLCL
      IMYMIILLGNSLLIITILDSRLHTPMYFFLGNLSFLDICYTSSSIPPMLIIFMSERKSISFIGCALQM
      VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLLQTVLT
      MMLPFCGNNVIDHITCEILALLKLVCSDITNVLIMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
  45  GRKKAFSTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
      KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)
```

```
      ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
      CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
      GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCCTGC
  50  TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
      TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGGAAACCTCTCATTCTTGGACAT
      CGTTACACATCCTCATCCATTCCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
      TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
      GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
  55  CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCCTGGATCATAGGCTG
      TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC
```

```
ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACTTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTCAGCGCACTCGATTGTGGTGATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG
TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)
```

AOLFR124 sequences:

```
MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLLTLAVV
DIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
YTFERDKVVAALYTLVTPTLNPMVYSFQNREMQAGIRKVFAFLKH (SEQ ID NO: 229)
```

```
ATGAATCACAGCGTTGTAACTGAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
AGGGAATTATCTTCCTCTTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTTCCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
GCTAACATCAGAAAATACCATTTCATATGCAGGCTGCATGTCCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTCACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTTCCCTCTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCCATTGCTGGCTTTG
TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCCACATTAAACCCGATGGTG
TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
CACTAG (SEQ ID NO: 230)
```

AOLFR125 sequences:

```
MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVIILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVVLLAGSEIGILTAMSYDRYAAICCPLHC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSKEHAI
ISVSVAIGVCYAFSCLVCIVVSYVYIFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL
KPGSDAPSILDLLVSVFYSVAPPTLNPVIYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID
NO: 231)
```

```
ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCCTCCG
ACATTTGTCCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
CTGTCGCCTCCACTGACTCCATCTCCTTCCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTGCCAGTTGATGGC
TCTGTCCTGGCTCAACAGAGGGGCCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG
AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
CACTTGTTCTAAAGAACATGCCATCATTAGTGTGTCAGTGTGGCCATTGGGGTCTGTTATGCA
TTTCATGTTTAGTTTGCATTGTAGTTTCCTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTCGCACCTCCAACCTTGAACCCTGTTATCT
```

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5   MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRLTFCNSNIIQHFYCDII
PLLKISCTDSSINFLMVFIFAGSVQVFTIGTILISYTIILFTILEKKSIKGIRKAVSTCGAHLLSVSLY
YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
10   NO: 233)

ATGTTCCTTTACCTTTGCTTCATTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
ACCGCTCTTCCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
15   TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
GCCTTTGTGGTAGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTCTGAATGCATGGTACAATTTTTTTCCCTTGTAACCACT
GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTCAGCTATTAGTCTTGTCA
20   TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTCATTCAGATTAACCTTCTG
TAATTCCAACATAATACAACACTTTTACTGTGACATTATCCCATTGTTAAAGATTTCCTGTA
CTGATTCCTCTATTAACTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTTACCA
TTGGAACTATTCTTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
25   ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGAGAT
GATGGAGTCTCTATTTTACACTGTCATAGTTCCTTTATTAAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID
NO: 234)

30   **AOLFR127 sequences:**

MSNEDMEQDNTTLLTEFVLTGLTYQPEWKMPLFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHFYCDIIPLFMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLLSVSLYYGPLIF
35   MYLRPASPQADDQDMIDSVFYTIIIPLLNPIIYSLRNKQVIDSFTIKMVKRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTTCTCACA
GGACTTACATATCAGCCAGAGTGGAAAATGCCCCTGTTCTTGGTGTTCTTGGTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACTTCAC
40   ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTTCCTTTGCATTGGTGGAACTACAGAATGTTTTCTCTTGGCAACAAT
GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTTTATTACCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA
45   TGAAGTCCTTATATTCAGATTAACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
ATATTATACCACTGTTTATGATTTCCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
TTTTGTCTGGCTCAATTCAGGTATTCAACCATTGTGACAGTTCTTAATTCTTACACATTTGCT
CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTTGCGCCCT
50   GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTCATTCACAAA
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55   METQNLTVVTEFILLGLTQSQDAQLLVFVLVLIFYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNLA
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMAFDRYIAICRPLHY

-136-

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNSGLLSLLCFLGLLASYAVILCRIREHSSEGKSKAISTCTTHIIIIFLMFGPAIFIYTCPFQAFP
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

5   ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
       AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
       AATTTCCTCATCATTTTCACCATAAAGTCAGACCCTGGGCTCACAGCCCCCCTCTATTTCTT
       TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCCCAGGATGTTG
       GTGGACTTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
10   TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCCTCCTCGTTGTGATGGCCTTTGACCGCTAC
       ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
       TATCGTTGGTTCTGTGGCTTGGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
       CACTTGCCTTTCTGTGGCCCAAʹACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
       CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCTG
15   CTCAGCCTCCTGTGCTTCCTGGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCGTATAAG
       GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
       ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCCTTCCAGGCTTTCCCAGC
       TGACAAGGTAGTTTCTCTTTCCAAACTGTCATCTTTCCTTTGATGAACCCTGTTATTTATA
       CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
20   CTGA (SEQ ID NO: 238)

       AOLFR129 sequences:

       MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI
       YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
25   QIFLLHLLGGVEMVLLVSMAFDRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
       AVNLPFCGPNVVDSIFCDLPLVTKLACIDIYFVQVVIVANSGIISLSCFIILLISYSLILITIKNHSPT
       GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTITPILNPIIYTLRNKEMKISMK
       KLWRAFVNSREDT (SEQ ID NO: 239)

30   ATGGCTCTTTATTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
       TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGTC
       AGAATTCATTTTGCTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTCTTGCTCCTCT
       TCTCGGTTATCTATGTGGTCACAGTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAC
       ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTTGTAGATATGAC
35   CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACTTGTTAAAAAAGCAGAAGGTAATT
       TCTTTTGCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
       ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCCATTTGTAAGCCCCTACACTACATG
       ACCATCATGAACAAGAAGGTATGTGTTTTGCTGTGAGTGACCTCATGGCTCTTGGGTCTCC
       TTCACTCAGGGTTTCAGATACCATTTGCTGTGAACTTGCCCTTTTGTGGTCCCAATGTGGTA
40   GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTTGT
       ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTTCATTATTTTGCTTA
       TCTCCTACAGTCTGATCCTCATAACCATTAAGAACCACTCTCCTACTGGGCAATCTAAAGC
       CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTGGCCCATGCATCTTTA
       TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATAACCATC
45   ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
       TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGTACTTAG (SEQ ID NO: 240)

       AOLFR131 sequences:

       MASTSNVTELIFTGLFQDPAVQSVCFVVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
50   LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
       ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
       NSGLFSVFSFLILVSSYIVILVNLRNHSAEGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
       KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

55   ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
       TGCAGAGTGTATGCTTTGTGGTGTTTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

                                      -137-

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCTAAATTCATCATAGAC
TTACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
5   ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTCACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCTCATCTTGGTGTCCTCTTATATTGTCATTCTGGTCAACTTGAGGAACCAT
10   TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

15

AOLFR132 sequences:

MVATNNVTEIIFVGFSQNWSEQRVISVMFLLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRKVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLLHSVGQTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT
20   FFISLLIITNGGSISVVSFFVLMASYLIILHFLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
25   CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
30   AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATCACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCCTACCTGATCATCCTGCACTTCCTGAGAAG
CCACAACTTGGAGGGGCAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTCACAGTTGTC
35   GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTGTCACCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

40   **AOLFR133 sequences:**

MTEFIFLVLSPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVLFFGPCVFNSLRPSTTLPI
45   DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTTCCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCCTCAGCTACCTCTCCTTCATGGA
50   GATCTGCTACTCCTCCGCTACAGCCCCCAAACTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
GATTTTCCTGCTCACTGTGATGGCCTATGACCACTACGTGGCCATCTGCAAGCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTACTGTCCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
55   TGTGATCAATCACTATTTCTGTGACCTAGTTCCCCTTCTCAAACTTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTTGGGGT

-138-

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFPTRPAFQLLFFSIFLATYLLTLLENLLILAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIAQLHYCGMPQINHYFCDISPLLNVSCE
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQGNGAFS
S (SEQ ID NO: 247)

ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTTCTGGAGATGTGGTATGTCACAGTCATC
AGCCCCAAGATGCTTGTTGACTTCCTCAGTCATGACAAGAGTATTTCCTTCAATGGCTGCA
TGACTCAACTTTACTTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGTTGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTTATAGCAACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
CTTCTTGGCCCTCCATGGTCATTGCTATTCCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCCTCCCACCTGACCGTCGTAATTCTCTTCTTCTTCTTCTTCATGCACTTTTCACCTATGCCCGTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTCACACTGTCATTGTT
CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSCTNTRVYEKVLLGVVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPQ
T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
GCACCATCCTGACTGAATTCATCTTGTTGGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTCAGGAAACATGACCTTGGTTA
TCTTAATCCGAACTGATTCCCACTTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
TTTTTGGATTTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
AGATAAGCGCATTTCCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTTCCTGTGTTTGTAGGCT
ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTGTAACCC
ATTGCTTTATTCAGGTACCATGTCACCGCCCTCTGTACTGGGCTTGTTGCTGGCTCCTACA
TAGGAGGATTTTTGAATGCCATAGCCCATACTGCCAATACATTCCGCCTGCATTTTTGTGG
TAAAAATATCATTGACCACTTTTTCTGGTGATGCACCATTGGTAAAAATGTCCTGTACA
AACACCAGGGTCTACGAAAAAGTCCTGCTTGGTGTGGTGGGGCTTCACAGTACTCTCCAGCA
TTCTTGCTATCCTGATTTCCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCCACCTCATCTCAGTCATGCTCTTCTA
TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCTAGAGAGGGACAAA
GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5   MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVIQPKMLVNFLGKKNTILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAAFFLGFLSALTHTSAMMKLSFCKSHIINHYFCDVLPLLNLSCSNT
HLNELLLFIIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSSHLMAVVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10

ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
CAGAGCTCCAGCTGCCCCTCTTCCTCCTGTTCCTGGGAAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCCTTCGTCGATTTCTGCTATTCCTCTGTGTCATTACTCCCAAAATGCTG
15   GTGAACTTCCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATACAAGTGCCATGATG
AAACTGTCCTTTTGCAAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCTCCT
20   CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCACCCTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
25   TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

MSPENQSSVSEFLLLGLPIRPEQQAVFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
30   LALTDISFSSVTVPKMLMNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP
PSSNTNDKNIIASVIYTAVTPMLNPFIYSLRNKDIKGALRKLLSRSGAVAHACNLSTLGG (SEQ
ID NO: 253)

35

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCCTGGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
40   TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTCACAGACATATT
TTTTCATATTTTTTGCTGACTTAGACAGTTTCCTTATCACTTCAATGGCATATGACAGGTAT
GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
TGGTGGCTGGGTCCTGGGTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCCTGGCC
45   CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
50   CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACTCTTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIVFLVVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
55   FVDVWFSSNVTPKMLENLFSDKKTISYADCLAQCFFFIALVHVEIFILAAIAFDRYTVIGNPLLY
GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFYCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILIAILRMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGKMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

```
      ATGCTCAATTTCACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGGAAT
 5    GGCAAGTTCTCTTCTTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
      GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTTCCTCA
      GTCACTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT
      CTGTTATCAGATAAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTTTCTTCTTCAT
      TGCTCTTGTCCATGTGGAAATTTTTATTCTTGCTGCGATTGCCTTTGATAGATACACAGTGA
 10   TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTCGACTGATTAC
      TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
      ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
      GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCAATTCTGCCGGCATCAACTTC
      ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
 15   GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
      CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
      GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
      TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
      GTTAA (SEQ ID NO: 256)
 20
```

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILILIIINKEAALHQPMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMAIDRYVAICRPLRYPSIITESFVFKAN
GFMALRNSLCLISVPLLAAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS
 25 DLGLIILSYALILYSVLKLNSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

```
      ATGGGATTCCCTGGCATTCACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT
 30   ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
      GCACCAGCCTATGTACTATTTCCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
      ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
      AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
      CTGCATGGCTATTGATAGATATGTAGCCATTTGTCGACCGCTACGATATCCATCAATCATC
 35   ACTGAATCTTTTGTTTTCAAAGCAAATGGGTTCATGGCACTGAGAAACAGCCTGTGTCTCA
      TCTCAGTGCCTCTGTTGGCTGCCCAGAGGCATTACTGCTCCCAGAATCAAATTGAGCACTG
      TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
      AACCAGGTCCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT
      ATGCTCTAATACTTTACTCTGTCCTGAAGCTGAACTCTCCAGAAGCTGCATCCAAGGCCTT
 40   AAGTACCTGCACCTCCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATTT
      CCATTACTCGTAGTACAGGAATGAGAGTTCCCCTTATTCCAGTTCTACTTAATGTGCTACA
      CAATGTCATTCCCCCTGCCCTGAACCCCATGTATATGCACTCAAGAACAAGGAACTCAGG
      CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAAGGGCCACCTGA (SEQ ID NO: 258)
```

AOLFR140 sequences:

MLTLNKTDLIPASFILNGVPGLEDTQLWISFPFCSMYVVAMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMLMALDRYV
 45 AICYPLRYSTILTNPVIAKVGTATFLRGVLLIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSSADARQKAFNTCTAHICAIVFSYTPAF
FSFFSHRFGEHIIPPSCHIIVANIYLLLPPTMNPIVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
 50 ID NO: 259)

```
      ATGCTAACACTGAATAAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
      GACTGGAAGACACACAACTCTGGATTTCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT
      GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAAACCATG
 55   TACTACTTCTTGGCCATGCTTTCCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
      AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG
```

```
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTCCT
CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
```
5
```
TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCCTGATTGGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
GCAGTGGTCAGCCTCCTCCTCAGCAGATGCTCGGCAGAGAAGGCCTTTAATACCTGCACTGCCC
ACATTTGTGCCATTGTTTTCTCCTATACTCCAGGTTCTCTCCTTCTTTTCCCACCGCTTTG
GGGAACACATAATCCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
```
10
```
CCCACTATGAACCCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)
```

AOLFR141 sequences:

```
MSSTLGHNMESPNHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVL
```
15
```
HKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM
AFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFLIGRLNFCQSHVILHTYCEHMA
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQSGQ
GMGIKASE (SEQ ID NO: 261)
```
20
```
ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
TCTTCTTCCTCCTGGGCATCCCAGGTCTGGAACAATTTCATTTGTGGCTCTCACTCCCTGTG
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
AACCAGTCTTGCACAAGCCTGTGTACCTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
```
25
```
GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
CAATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACTTCTGCCAAAGCCATGTGATCC
```
30
```
TACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCATTGG
TCTCTCCTATGCCCTAAGTGCACAAGCTGTCCTTCGCCTCTCATCCCATGAAGCTCGGTCCA
AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACCAGCCCTC
TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGAC
```
35
```
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC
AGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)
```

AOLFR143 sequences:

```
MLGLNGTPFQPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMYYFL
```
40
```
SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
HVNNIYGLLVIIFTYGMDSTFILLSYALILRAMLVIISQEQRLKALNTCMSHICAVLAFYVPIIAVS
MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKEIRKGILKFFHKSQA (SEQ ID NO: 263)
```
45
```
ATGTCTGGGTCTCAATGGCACCCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCCTG
GGATACAAACAGGCCTCACCTGGGTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
GTAGGTAACCTCAGCATTCTCACTCTGGGTTTGGGAGCCTGCTCTGCATCAGCCCCCATGT
```
50
```
ACTACTTCCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCCTTTTCTACACTTCCCACT
GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACCACTCTCTTCCCTTTCCCTTTTGTGGT
```
55
```
GAAACGACTGCCCTTCTGCAAAGGCAATGTTTGCATCACTCCTACTGTCTCCATCCAGAT
CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
```

```
    TTTTTACCTATGGTATGGACTCAACTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
    ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
    TCTGTGCAGTGCTGGCCTTTTATGTGCCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
    AAAAGTGCTCACCCTGTTGTTCATGTCATGATGTCCAATGTCTACCTGTTTGTACCACCCAT
  5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
    TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)
```

AOLFR144 sequences:

```
     MGLFNVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFL
 10  SMLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
     PLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
     NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
     TVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)
```

```
 15  ATGGGGTTGTTCAATGTCACTCACCCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA
     GAGCTCTCACTCCTGGCTGTCAGGGCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
     AATACAGTGATCCTGCAGGCTGTGCGAGTTGGAGCCCAGCCTCCATGAGCCCATGTACTACT
     TCCTGTCCATGTTGTCCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
 20  CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
     TATTCACTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
     TGGCCATTTGTGACCCCTTGCGCTATGCAACTGTGCTCACCACTGAAGTCATTGCTGCAAT
     GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCCTTTTCCCTCTTCCCTTTCTTATTAAGA
     GGCTGCCTATCTGCAGATCCAATGTTCTTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 25  AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC
     CTTTGGCATGGACCTGTTTTTTATCTTCCTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG
     CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
     TGTACTTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
     GTCCCATGCTACATACATGTCCTCATGTCAAATGTGTACCTATTTGTGCCTCCTGTGCTCAA
 30  CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
     CACATCAAAAATGA (SEQ ID NO: 266)
```

AOLFR145 sequences:

```
     MSVQYSLSPQFMLLSNITQFSPIFYLTSFPGLEGIKHWIFIPFFFMYMVAISGNCFILIIIKTNPRLH
     TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
 35  RFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIPIVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
     CTDTTFNNLYGLMVVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
     FVPMMGLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIIKLLGLKKASK
     (SEQ ID NO: 267)
```

```
 40  ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
     CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
     CCTTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
     ACCAACCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
     GGGGCTGTGTGTGTCCACGTTGCCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 45  ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTTCCTTCATGGAGTC
     CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT
     CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
     TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTCCCTACTGTGGATCTGTGGTCC
     TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
 50  CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGCTCATC
     GCACTGTCCTATGGACTCATCCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
     GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
     ATGGGGCTGTCCCTGGTGCACCGTTTTGGGAAGCATGCCCCACCTGCTATTCATCTTCTTAT
     GGCCAATGTCTACCTTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
 55  AAGGAGATCCACCGTGCCATTATCAAACTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
     ID NO: 268
```

                                        -143-

AOLFR146 sequences:

MSQVTNTTQEGIYFILTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMYLFLSM
LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP
LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
SWYGFALALLIIIVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT
HRFAKHASPLVHVIMANTYLLAPPVMNPIIYSVKNKQIQWGMLNFLSLKNMHSR (SEQ ID NO:
269)

ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
ATGGGCAATACCACCATCCTCACTGTCATTCGCACAGAGCCATCTGTCCACCAGCGCATGT
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCTCACCACCCTACCCACA
GTCATGCAGCTTCTCTGGTTCAACGTTCGTAGAATCAGCTCTGAAGCCTGTTTTGCTCAGTT
TTTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCCTCCTGGCTATGTCCGTTGACT
GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTTGCTCTTGCCTT
GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTTATTCTGAAAAATA
TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCCACAT
TCTAGCTGTCCTGGTCCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
GATGAACCCCATCATTTACAGTGTAAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTC
CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNCILLYLIVVEHSLHEPMF
FFLSMLAMTDLILSTAGVPKALSIFWLGAREITFPGCLTQMFFLHYNFVLDSAILMAMAFDHYV
AICSPLRYTTILTPKTIIKSAMGISFRSFCIILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
NFWYGFCVPIMTVISDVILIAVSYAHILCAVFGLPSQDACQKALGTCGSHVCVILMFYTPAFFSI
LAHRFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:
271)

ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATTCCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTTCTCTCCACTGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC
CAGGATGCCTTACACAAATGTTCTTCCTTCACTATAACTTTGTCCTGGATTCAGCCATTCTG
ATGGCCATGGCATTTGATCACTATGTAGCTATCTGTTCTCCCTTGAAGATATACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGCTGACATGCTGCCTTTCTGCAGGACACGCATCATACCCCACA
CATACTGTGAGCATATAGGTGTTGCCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCCT
ACGCACACATCCTCTGTGCTGTCTTTGGCCTGCCTTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTTCTCCA
TCCTCGCCCATCGCTTTGGACAAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTTATACTTTTGTTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLGLQDQHMWISIPFFISYVTALLGNSLLIFIILTKRSLHEPMYLFLC
MLAGADIVLSTCTIPQALAIFWFRAGDISLDRCITQLFFIHSTFISESGILLVMAFDHYIAICYPLR
YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

-144-

FSILMSTVVLDVVLFISYMLILHAVFHMPSPDACHKALNTFGSHVCIIILFYGSGIFTILTQRFGR
HIPPCIHIPLANVCILAPPMLNPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

```
     ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
  5  GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCTTCATTTCCTATGTCACCGCCCTT
     CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
     ACCTCTTCCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
     GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
     CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGACAGGCCTTTGACC
 10  ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCTTACAAATGCTCTGATCAA
     GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
     TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCCACACACCTTTTGTGAACACATTGG
     CCTAGCCAAATATGCATGTAATGACATTCGAATAAACATTTGGTATGGGTTTTCCATTCTA
     ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCCTATATGCTGATTCTCCATGC
 15  TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
     TCTGCATCATCATCCTCTTTTATGGGTCTGGCTTTCAACAATCCTTACCCAGAGGTTTGGA
     CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
     GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
     TTGTTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)
 20
```

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL
SFIDMWFSTVTVPKLLMTLVFPSGRAISFHSCMAQLYFHFLGGTECFLYRVMSCDRYLAISYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWIQHYLCDAPPILKLACADTS
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFQTCASHCIVVLCFFGPGLFIYLR
PGSRKAVDGVVAVFYTVLTPLLNPVVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

```
     ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
 30  TGGACGCCCCCCCTCTTTGGAGTCTTCCTGGTGGTTTTACGTGCTCACTGTGCTGGGGAACCT
     CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCCTCA
     CCAACCTGTCGTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC
     TTTGGTGTTCCCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT
     TTCACTTCCTAGGGGGGCACCGAGTGTTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT
 35  GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
     GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
     ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT
     GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
     GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCT
 40  GCGGATCCGCACCTCAGAGGGGAAGCACCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
     GTGGTCCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGAAAGC
     TGTGGATGGAGTTGTGGCCGTTTCTACACTGTGCTGACGCCCCTTCTCAACCCTGTTGTGT
     ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
     ATTCTCAGAGCAAATAG (SEQ ID NO: 276)
 45
```

AOLFR150 sequences:

MELGNVTRVKEFIFLGLTQSQDQSLVLFLFLCLVYMTTLLGNLLIMVTVTCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSCMTQIFLFHLLGGADIFSLSVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGDPAFCALHLCLC
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

```
     ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
     AAGACCAGAGTTTGGTCTTGTTTCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
 55  AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCCATGTACTTCCT
     GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACTGCTCCTAAAGTCTTGC
```

TGGACCTTCTGTCAAAGAAAAAGACCCATATCCTATACAAGCTGCATGACACAGATATTTCT
CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTCTGTGATGGCGTTTGACTGCTACA
TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
CATCTCTGCCTCTTGGATGGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
5   CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
AAACTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT
CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCCTACACAGTCATCCTAATGACGCTGAGGT
CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGCACCTCCCCACATCACTGTG
GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGACCCGGCCCTTCACTGCCCTCCCCAC
10   AGAAAAGGCCATCTCTGTCACCTTCACTGTCATCTCCCCTCTGCTGAACCCTTTGATCTACA
CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15   MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHLS
FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMALDRYVAICSPLHYS
SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLFCMYVRPPSE
KSVEESKITAVFYTFLSPMLNPLIYSLRNTDVILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

20

ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCCTTGCGATCTACCTAATCACACTGGCAGG
CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTC
TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
25   GCACAATTTCCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
CTCTTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
TCACTTATCCTTCTGTGGCTCCCTTGAAATCAAATCATTTCTACTGCGCTGATCCTCCTCTTA
30   TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
TAATCTCTCAAGCTCTCTCTTCATCATTCTTCTGTCCTATCTTTTCATTTTTGCAGCGATCTT
CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACCTGACA
ATAGTCACTTTGTTTTATGGAACCCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTATCTTTGAGCCCAATGCTGAACCC
35   ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

40   MDQINHTNVKEFFFLELTRSRELEFFLFVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCMAQIFFFHFAGGADIFFLSVMAYDRYLAIAKPL
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
FALELFMISNNGLVTLLWFLLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPVCV
YIYCRPFMTLPMDTTISINNTVTIPMLNPIIYSLRNQEMKSAMQRLQRRLGPSESRKWG (SEQ ID
NO: 281)

45

ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCCTGGAACTTACACGTTCCC
GAGAGCTGGAGTTTTTCTTGTTTGTGGTCTTCTTTGCTGTGTATGTAGCAACAGTCCTGGG
AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
50   GTGGATCTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTTCCTCTCTGTGATGGCCTATGACAGATAC
CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCTTCATTCAATCATCAATCAGGTAATTCTGATGC
TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
55   GTAAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
TGGTGACCCTGCTCTGGTTCCTCCTGCTCCTGGGCCTCCTACACTGTCATTCTGGTGATGCTG

```
     AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
     GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
     CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCCATGCTGAACCCCATCATC
     TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
   5 CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)
```

AOLFR153 sequences:

```
     MSKTSLVTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
     FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
  10 RYTSMMSGSRCALLATSTWLSGSLHSAVQTILTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
     NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR
     PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLRDKVAHSQGE (SEQ ID NO:
     283)
```

```
  15 ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
     TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
     CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
     CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
     CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
  20 TCCACTTCCTGGGGAGCACCGAGTGTTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
     GCCATCAGTTACCCGCTCAGGTACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
     CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
     TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA
     AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTTGGACATTGGGCTAGT
  25 GGCCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
     GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
     GGTCCTTTGCTTTTTTGTNNCCTGTGTGTTTTCATTTACCTGAGACCAGGCTCCAGGGACGTCG
     TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC
     ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
  30 TCTCAGGGAGAATAA (SEQ ID NO: 284)
```

AOLFR156 sequences:

```
     MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIIIDNLLIFSAVRL
     DTHLGNPMYNFISIFSFLEIWYTTATIPKMLSNLISEKKAISMTGCILQMYFFHSLENSEGILLTT
  35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP
     VLSLACTDTSMILIEDVIHAVTIIITFLIIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
     SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
     (SEQ ID NO: 285)
```

```
  40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
     ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
     CCTGTACTTCTTTCCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
     CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
     CCTTTCTGGAGATCTGGTACACCACAGCACCATTCCCAAGATGCTCTCCAACCTCATCAG
  45 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT
     GAAAACTCAGAGGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
     ACCCTCTTCGCTATCAAATGATCATGACCCCCGTGCTTGGTCCCACCTCTCTGCAGGTTCC
     TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG
     TGGGCCCAACCAAATCCATCAGATCTTTCTGTGACTTGGTCCCTGTGCTGAGCCTGGCCTGT
  50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCATGCTGTGACCATCATCATTACCT
     TCCTAATCATTGCCCTGTCCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
     GAAGGGAGGCAAAAGGCTNTTTCTACCTGTGCAGGCCACCTCATGGTCTTCCTGATATTCT
     TTGGCAGTGTATCACTCATGTACTTGCGTTTCAGCAACACTTATCCACCAGTTTTGGACAC
     AGCCATTGCACTGATGTTTACTGTACTTGCTCCATTCTTCAATCCCATCATTTATAGCCTGA
  55 GAAACAAGGACATGAACAATGCAATTAAAAAACTGTTCTGTCTTCAAAAAGTGTTGAACA
     AGCCTGGAGGTTAA (SEQ ID NO: 286)
```

AOLFR157 sequences:

MAMDNVTAVFQFLLIGISNYPQWRDTFFTLVLIIYLSTLLGNGFMIFLIHFDPNLHTPIYFFLSNL
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
5   LRYSVVMNGPVCVCLVATSWGTSLVLTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
NEFMILITSIFTLLLPFGFVLLSYIRIAMAIIRIRSLQGRLKAFTTCGSHLTVVTIFYGSAISMYMKT
QSKSSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTTCAGTTTCTCCTTATTGGCATTTCTAACTATCC
10 TCAATGGAGAGACACGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC
TCCTTGGCTTTGGCCACAGCAGAGTGCCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
15 TTGCTATCAGCAATCCCCTGCGTTATTCAGTGGTTATGAATGGCCCAGTGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTAA
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCACCAGTATCTTCACCC
TGCTGCTACCATTTGGGTTTGTTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACTCAGTCCAAGTCCTCCCC
TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCCTG
ATATATAGCCTGAGAAAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
ACATGA (SEQ ID NO: 288)

25

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFMLFLSMYLATMLGNLLILAVNSDSHLHTPMYFLLSI
LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFVGLENGILVMMAYDRFVAICHP
30 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCELAHILKLACSDVLIN
NILVYLVTSLLGVVPLSGIIFSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCCTGTCCATGTACCTGGCCACAATGCTGGG
35 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACAAGCCCTCCAATCTCC
TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTCACCTCCACCACGATGCCCAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
TTGTCCTGGTTTTTGTTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
40 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCCTTGGATGCTCTGCTGCACACGTTGATGGTGCT
ACAGCTGACCTTCTGCATAGACCTGGAAATTCCCCACTTTTTCTGTGAACTAGCTCATATTC
TCAAGCTCGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
GTTAGGTGTTGTTCCTCTCTCTGGGATCATTTTCTCTTACACACGAATTGTCTCCTCTGTCA
TGAAAATTCCATCAGCTGGTGGAAAGTATAAAGCTTTTTCCATCTGCGGGTCACATTTAAT
45 CGTTGTTTCCTTGTTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGGCTACCCACT
CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCCATGCTGAACCC
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAAACTAATATCTAG
GATACCATCTTTCCATTGA (SEQ ID NO: 290)

50 **AOLFR159 sequences:**

MGPRNQTAVSEFLLMKVTEDPELKLIPFSLFLSMYLVTILGNLLILAVISDSHLHTPMYFLLFN
LSFTDICLTTTTVPKILVNIQAQNQSITYTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHPL
RYTVLMNVHFWGLLILLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
55 INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMPSARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
SAVAESSRITAVASVMYTVVPQMMNPFIYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

-148-

ATGGGACCCAGAAACCCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
CCAGAACTGAAGTTAATCCCTTTCAGCCTGTTCCTGTCCATGTACCTGGTCACCATCCTGG
GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC
CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT
5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT
CTTGTCTTGGTTTTTGCTGGCTTGGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
CTGATTCTTCTCTCCATGTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTCAGGTC
10 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTC
TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTCCACCTGTGGCTGTCACCTCTC
TGTTTTTTCCTTGTTCTATGGGACAGCTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
15 CTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGGAAACTTATTGGTAG
GCTGTTTCCTTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

20 MPMQLLLTDFIIFSRIFIINSMEARNQTAISKFLLLGLIEDPELQPVLFSLFLSMYLVTILGNLLILL
AVISDSHLHTPMYFFLSNLSFLDICLSTTTIPKMLVNIQAQNRSITYSGCLTQICFVLFFAGLENC
LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLLTSVVNALLLSLMVLRLSFCTDLEIPLFF
CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGIILSYTQITSCVLRMPSASGKHKAVSTCGSHL
SIVLLFYGAGLGVYISSVVTDSPRKTAVASVMYSVFPQMVNPFIYSLRNKDMKGTLRKFIGRIP
SLLWCAICFGFRFLE (SEQ ID NO: 293)

25

ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
CATGGAAGCGAGAAACCAAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT
CCGGAACTGCAGCCCGTCCTTTTCAGCCTGTTCCTGTCCATGTACTTGGTCACCATCCTGGG
GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
30 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTCTTAAGCACAACCACGATCCCAAAGATGCTG
GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT
TTGTCTTGTTTTTTGCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
GTGGCCATTTGTCACCCCCTTAGATACACAGTCATCATGAACCCCCGCCTCTGTGGCCTGC
TGATTCTTCTCTCTCTGTTGACTAGTGTTGTGAATGCCCTTCTTCTCTCAGCCTGATGGTGTTG
35 AGGCTGTCCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAACTGGCTCAGGTCA
TCCAACTCACCTGTTCAGACACCCTCATCAATAACATCCTGATATATTTTGCAGTCAGTGCATA
TTTGGTGGTGTTCCTCTGTCTCGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
GAGAATGCCATCAGCAAGTGGAAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
ATTGTTCTCTTGTTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTCAGGTTTCTAGAGTAA (SEQ ID
NO: 294)

45 **AOLFR161 sequences:**

MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMVVGNLLILAISIDSHLHTPMYFFLANL
SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
50 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFSTCSSHLSVVALFYGTTIGVYLCP
SSVLTTVKEKASAVMYTAVTPMLNPFIYSLRNRDLKGALRKLVNRKITSSS (SEQ ID NO: 295)

ATGGAACCAAGAAACCCAAACCAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
CAGAGCAGGAGACGCTTCTCTTTTCCTGTTCTTCTGTATGTACCTGGTCATGGTCGTGGGG
GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT
55 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

-149-

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTCGCCTG
CTGGTCGGCGCCCTCTGGGCGTTTTCCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC

5   TCCGACTTTCGTGCACGGACACCTCGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA
TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
TGTGGTTGCTCTCTTCTATGGGACCAACCATTGGCGTCTATCTGTGTCCCCTCCTCGGTCCTCA

10 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
CTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH

15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
YDRYAAIWNPLLYPVLVSGRICFLLIATSFLAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
LKLSLSCSDTHFNGIVIMAFSSFIVISCVMIVLISYLCIFIAVLKMPSLEGRHKAFSTCASYLMAVTIF
FGTILFMYLRPTSSYSMEQDKVVSVFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
NO: 297)

20
ATGATGAGACTTATGAAAGAGGTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
CTCCACACCCCATGTATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT

25 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCCTGGGGACTGAGTGCTTCCTGTTGGCC
ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCCTGCTCTACCCAGTTCTCGTGT
CTGGGAGGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
CATACATACAGGGATGACTTTTAGGTTGTCCTTTTGTGGTTCTAATAGGATCAACCATTTCT

30 ACTGTGACACCCCGCCACTGCTCAAACTCTCTTGCTCTGTATCACCCACTTCAATGGCATTGTG
ATCATGGCATTCTCAAGTTTTATTGTCATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT
GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT
GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA

35 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCCC
TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN

40 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
LYAQAMSIKLCALLVAVSYCGGFINSSIITKKTFSFNFCRENIJDDFFCDLLPLVELACGEKGGYK
IMMYFLLASNVICPAVLLASYLFIITSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYIYALPRS
SYSFDMDKIVSTFYTVVFPMLNLMIYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
GGAATGCAGCTGGGCCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
ATAGCACCCTCATCGTGTTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTTCT

50 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
GGCCATCTCCAAGCCCCTGCTTTATGCCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
GTAGCAGTCTCATATTGTGGTGGCTTTATTAACTCTTCAATCATCACCAAGAAAACGTTTTC
CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTTGCTTCCCTTGGTGG
AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCCTGCTGGCCTCCAA

55 TGTCATCTGCCCCGCAGTGCTCATCCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCCACCTGACCTCT

-150-

GTCACTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAACTTCTCCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHFFCELSSLISLSYPDSYL
SQLLLFTVATFNEISTLLILTSYAFIIVTTLKMPSASGHRKVFSTCASHLTAITIFHGTILFLYCVP
NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

10

15   ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
ATTACCTGGAACTGCAAATTCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCCATGT
ATTTTTTCCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCCTCCATCATTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
20   CTTTTCTTTTGCACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
25   TTTTAATGAGATAAGCACACTACTCATCATTCTGACATCTTATGCATTCATCATTGTCACCA
CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCTTGTTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
30   ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTTGTTATTGAACAATA
A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
35   SNLSFLDICYVSSTAPKMLSDIITBQKTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
PLLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCELDLPPVLALSCSDTF
TSEVVTFIVSVVVGIVSVLVVLISYGYIVAAVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVVNPIIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

40   ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC
ATCCTCAAATGAAGATTTTCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
TGGAACTTAAGCCTCATTGCCCTCATTAAGATGGACTCTCACCTGCACATGCCCATGTACT
TCTTCCTCAGTAACCTGTCCTTCCTGGACATCTGCTATGTGTCCTCCACCGCCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAACCATTTCCTTTGTTGGCTGTGCCACTCAGTACT
45   TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTTAA
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCCTTAGTTCTTTCATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTTCTGTGACCTCCCTCCAG
TCCTGGCTCTGTCCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
50   GTCGTTGGAATAGTGTCTGTGCTAGTGGTCCTCATCTCTTATGGTTACATTGTTGCTGCTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCCAGCTA
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCTGTGGTGAAT
CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
55   AGGGACCCCGGGATTTCTCACGGTGGACCATTCATTTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSLVLFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
5   HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL
ELLMISNNGLLTTLWFFLLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP
FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAACTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
10   GGGAAGTGAGCTAGTCTTATTTCTTTTCCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTTCCATCACAGTGCCCAAGGTTCTGG
TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
15   TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC
CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCCT
CAAACTGGCCCATACAGACATTTTCATACTTGAACTACTAATGATTTCCAACAATGGACTG
CTCACCACACTGTGGTTTTTCCTGCTCCTGGTGTCCTACATAGTCATATTATCATTACCCAA
20   GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT
GGTGACCCTGCATTTCGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA
TGGATAAGGCCATCTCTGTCACCTTCACTGTCATCTCCCCTCTGCTCAACCCCTTGATCTAC
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
TCTGATAGAAAATAG *SEQ ID NO: 306)

25   **AOLFR167 sequences:**

MSITKAWNSSSVTMFILLGFTDHPELQALLFVTFLGIYLTTLAWNLALIFLIRGDTHLHTPMYFF
LSNLSFIDICYSSAVAPNMLTDFFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI
SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNIINFFFCDLPPVLALSCSDT
30   FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLLFGTAL
FVYLRPSSSYLLGRDKVVSVFYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
NO: 307)

ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTCATCCTCCTGGGATTCA
35   CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCCTAAGCAACTTATCTTTCATTGACATCTGCTACTCTTCCGCTGTCGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTTGTGGGCTGTGCTGCTC
AGTTTTTTTTCTTTGTCGGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATAC
40   GACCGATATGCAGCCATCTCCAGCCCCCTTCCTCTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGCGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCCTGGCTCTGTCTTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCCTCGTG
GTGGTCACTGTCGGAGGAACATCGTTCCTCCAACTCCTTATCTCCTATGGTTACATAGTGT
45   CTGCGGTCCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTTCGTGTACTTGCGACCCAG
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTCATTGGTGATCCCC
ATGCTGAACCCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAAGGAAGAAAGTGTTTTCTTAG (SEQ ID NO: 308)

50   **AOLFR168 sequences:**

MEKINNVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM
TIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETYIVG
55   VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD

TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

ATGGAAAAAATAAACAACGTAACTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTTTTGTGGTGTTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTIATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATTGGTGGCT
ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACT
ACCCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTCACCCTGTGTTGAAA
CTTGCCTGCACAGAAACATACATTGTTGGTGTTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTTGTTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCCACATTGCCATGGTCG
TTATCTTTTTCGGCCCCTGTACTTTTATGTACATGCGCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

AOLFR169 sequences:
MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFFYLVTLMGNTVIIVIVCVDKRLQSPMYFFLSHL
STLEILVTTIIVPMMLWGLLFLGCRQYLSLHVSLNFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLLKLSCDNTLLTEFI
LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTTGCTATATTCTTTTTCTTCTATTTAGTGACATTAATGGGAAAC
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCT
CAGCCACCTCTCTACCCTGGAGATCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG
GGATTGGCTCTTCCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTCAGTTTACCTTC
CGCAAATCAAATTCATTAGACCATTTTTACTGTGACCGAGGGCAATTGCTCAAACTGTCCT
GCGATAACACTCCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACCTTTTGCCTCCCACTTCACCTGTGTTGTGATTG
GCTATGGCAGCTGCTTGTTTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCCTTCCTGAATCCTTTCATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:
MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVIITTGCMVQFYFHFSLGSTSFLIL
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
FFCDNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILTFCNQTVKTVLQGGMQ
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTCT

```
           TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTTTCTCTTGCATGCAGGGCCCCATACTG
           TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG
           TGAGCTGCAGGCCCTTCTGTATGGCCCCTTCCTCATGCTTTATCTTCTCGCCTTCATGGGAA
           ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
5          CTGGGCAATTTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCCAGGATGCTCT
           CAGACCTGTTGGTCCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
           CACTTTTCCCTGGGGTCCACCTCCTTCCTCATCCTGACAGACATGGCCCTTGATCGCTTTGT
           GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGGCTATGTGTCCAGCTG
           GCTGGGGCTGCCTGGGCAGCTCCTTTCCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC
10         ATCTTGATTACTGGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
           CAGTIGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
           TGTCCTCAGCTCCTTCCTGGTGACCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
           GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT
           GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
15         GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCCTTTCTCAATCCCT
           TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT
           GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)
```

AOLFR171 sequences:

```
20         MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI
           EHLLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLLVVAMIGGFVHSVVQIVFLYSLP
           ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGICMVIFTFLLISCGVILNFLKTYSQEER
           HKALPTCISHIIVVALVFVPCIFMYVRPVSNFPFDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
           KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)
25
           ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCTCCTTGGGCTCCCTAA
           TGTACTTCTTCCTTGCCTACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCCACCC
           AAATTGATGATGAGACTTACTCTGTGATAAAATCGCTATTTCCTTGTCAGCTGCATGGGTC
           AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCCTTTTGGTGGTGATGGCCTA
30         TGATCGCTATGTGGCTATCTCTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
           TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT
           CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
           ACCCATTGTTGGAACTGTTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
           TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
35         ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
           CATCATTGTGGTTGCCCTCGTTTTTGTTCCCTGTATTTTATGTATGTTAGACCCGTTTCCA
           ACTTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
           TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
           AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACACTGAACATATTTATTCCTAGTTCTA
40         AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)
```

AOLFR172 sequences:

```
           MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
           FLLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
45         AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFPLLVAKFEHFQAKTIGHTYCAHMAV
           VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL
           AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
           (SEQ ID NO: 317)
50         ATGGCAGAAACTCTACAACTCAATTCCACCTTCCTACACCCAAACTTCTTCATACTGACTG
           GCTTTCCAGGGCTAGGAAGTGCCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTTATCT
           GCTGGCCCTGCTGGGCAATGGAGCACTGCCCGGCAGTGGTGTGGATGACTCCACACTGCA
           CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
           ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
55         GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
           CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCCTGGTCACC
```

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCCATACCTA
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
5   GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTCTCTCCAACAT
CTACTTGCTGCTGCCACCTGCCCTCAACCCCCTCATCTATGGGGCCCGCACCAAGCAGATC
AGAGACCGACTCCTGGAAACCTTCACATTCAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10   **AOLFR173 sequences:**

MSHTNVTIFHPAVFVLPGIPGLEAYHIWLSIPLCLIYITAVLGNSILIVVIVMERNLHVPMYFFLS
MLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGFFVHMMFVGESAILLAMAFDRFVAIC
15   APLRYTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
NIWYGFSVPIVMVILDVILIAVSYSILRAVFRLPSQDARHKALSTCGSHLCVILMFYVPSFFTLL
THHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGVAHRFFDIKTWCCTSPLGS
(SEQ ID NO: 319)

20   ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCCTTCCTGGCATCCCTGG
GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTTACATCACTGCAGTCC
TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA
TTTCTTCCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
CCCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTCACCCAAGGC
25   TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
CTTTGTGGCCATTTGTGCCCCACTGAGATATCAACAGTGCTAACATGGCCTGTTGTGGGG
AGGATTGCTCTGGCCGTCATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCTCACTCCTACTGTGAGCATATTGGA
GTGGCTCGTTTAGCCTGTGCTGACATCACGTTTAACATTTGGTATGGCTTCTCAGTGCCCAT
30   TGTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
TGTTTCGTTTGCCCTCCCAGGATGCTGGCACAAGGCCCTCAGCACTTGTGGCTCCCACCT
CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG
TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTTGGCAGTGCCACCAAGTC
TGAACCCCATTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCCACCGGTT
CTTTGACATCAAGACTTGGTGCTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35   **AOLFR175 sequences:**

MHFLSQNDLNINLIPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
40   SGCFLQFYFFFSLGSTECFFLAVMAFDRYLAICRPLRYPTIMTRRLCTNLVVNCWVLGFIWFLIPI
VNISQMSFCGSRIIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRAVL
RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVMYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

45   ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
TCATTCAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTAACCTCCTGACCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTCACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
50   CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCTCCAGTTCTACTTTTTCTTCTCC
TTGGGCTCTACAGAATGCTTTTTCCTGGCAGTTATGGCATTTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACCATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCCTATTGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTTCTAACTCTCACTTG
55   CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTTCTGTCTTAAGTCCTCTGCCTGTCTTTATGC
TCTTTCTCTTCATTGTGGGGTCCTATGCTCTGGTCGTGAGAGCTGTGTTGAGGGTCCCTTCA

GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCACCATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTTGGGGAACATAA (SEQ ID NO:
5   322)

AOLFR176 sequences:

MPFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGQREMQSCFFSFILVLYLLTLLGNGAIVC
10   AVKLDRRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTECFF
LSVMAYDRYLAICRPLHYPSIMTGKFCIILVCVCWVGGFLCYPVPIVLISQLPFCGPNIIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

15   ATGTTCTTTATTATTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTCATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCAGTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
20   AACTTTGCCTTTCTAGAGATCTGGTACATTTCCTCCACTGTCCCAAACATGCTAGTCAATAT
CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCCTGCAATTCTATTTCTTTTTTTC
ACTGGGTACAACAGAGTGTTTCTTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT
25   TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATTGTTTGCACTGGC
CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACAACCTTCAACTCGATGATTATCTTTG
GGCCCTTCCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGCTGGTCGAACTAAAGCTTTCTCCACATGTGGGTCCCACCTAATGGTGGTGTCTC
TATTCTATGGAACCCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
30   GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCCTTATCTAT
AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGC
CAAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLFSLFLVIYVLTLLGNGAIIYAVRCNPLLH
35   TPMYFLLGNFAFLEIWYVSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTECLFLAVMAYD
RYLAICHPLQYPAIMTVRFCGKLVSFCWLIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLLTAVFQVPSAAGRRKAFSTCGSHLVVVSLFYG
TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRIRQNS
(SEQ ID NO: 325)
40

ATGTCTTCTTCTTTGTAGACTTAAGACCCCATGAACAGGTCAGCAACACACATCGTGACAG
AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTCAGATTTTCCTCTTCTCATTGTTT
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
ACCCACTACTACACACACCCCCATGTACTTTCTGCTGGGAAATTTTGCCTTCCTTGAGATCTGG
45   TATGTGTCCTCCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAAGGCCATCTC
ATTTTCTGGGTGCTTCCTCCAGTTCTATTTCTTCTTTTCACTGGGAACAACTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCCTTG
GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCCTTCTGTGGTCCTAATATCATTGAT
50   CACTTCCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCATAACTG
AATGTATTTTCTATACTCAGAGCTCCCTTGTCCTCTTTTTCACTAGTATGTACATTCTTCGA
TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAAG
CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
ATGTATGTAAGTCCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACTCTGGTAT
55   ATTCAGTAACGACTCCTCTTTTTAATCCTCTGATCTATACTCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGGAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO:
326)

AOLFR178 sequences:

MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIAQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
LQYLTIMSPRMCMFFLVAAWVTGLIHSVVQLVFVVNLPFCGPNVSDSFYCDLPRFIKLACTDSY
RLEFMVTANSGFISLGSFFILIISYVVIILTVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

ATGGTTGGGGCAAATCACTCCGTGGTGTCAGAGTTTGTGTTCCTGGGACTCACCAATTCCT
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTTGCTCACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTTCT
GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCCTCTGTCACTTCTCCCAAAATGATTT
ATGACCTGTTCAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT
GTGGCCATATGTAAGCCCCTCCAGTACCTGACCATTATGAGCCCAAGAAATGTGCATGTTCT
TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
AACTTGCCCTTCTGTGGTCCTAATGTATCGGACAGCTTTTACTGTGACCTTCCTCGGTTCAT
CAAACTTGCCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC
ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCCTATGTGGTCATCATTCTCACTGTTCT
GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCACGTCAGTGTG
GTAGTTTTGTTCTTTGGTCCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA
CATTCAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

MNGMNHSVVSEFVFMGLTNSWEIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
LHYLTIMSPRMCLYFLATSSIIGLIHSLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
EFMVTVNSGLISVGSFVLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
PSPSTHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTCATGGGACTCACCAACTCAC
GGGAGATTCAGCTTCTACTTTTTGTTTTCTCTTGTTGTTCTACTTTGCGAGCATGATGGGA
AACCTTGTCATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCCT
CCTGGCTAACCTCTCAATCATTGATATGGCATTTTGCTCAATTACAGCCCCTAAGATGATT
GTGATATTTCAAGAAGCACAAGGCCATCTCCTTTCGGGGATGTATTACTCAGATCTTCTT
TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
ATGGCCATATGTAAACCTCTCCACTACCTGACCATCGAGCCCAAGAATGTGTCTGTATACT
TTTTAGCCACTTCCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
GATTTACCTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTCATCTCCCTCGGCTCCT
CAGACTTGCCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCCTACATCTTCATTCTGTTCACTGTTTG
GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCACTGTG
GTCATCTTGTTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCCACATCACACCT
GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
CATTCAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
TTACAAAGATTTTGTAA (SEQ ID NO: 330)

AOLFR180 sequences:

MTNKMYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSSNFLLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRRLHKPMYYFLSMLAAVDLCLTITTLPTVLGVLWFHAREISFKACFIQMF
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLLPLLVAINTVSF
HGGHELSHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGTDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR
QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)


```
     ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT
  5  TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCCTCAAACTTCC
     TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
     CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCATCATTACTAAGCGGA
     GACTCCACAAACCCATGTATTATTTCCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
     ATTACGACCCTTCCCACTGTGCTTGGTGTTCTCTGGTTTCATGCCCGGGAGATCAGCTTTAA
 10  AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCTCGGTGCTGG
     TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCACTGAACTATGCTACTATCCTC
     ACAGACAGGATGGTCCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
     TTCCCCTTCTTGTAGCCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
     TTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
 15  GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCCTAT
     GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA
     GCACTTGTGTCTGTCACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
     TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCGTGAGCACTTTGGCCCAATATTTA
     TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTGAAGACCAAGACAATCCGC
 20  CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
     GGGGAAGATGGGATTGA (SEQ ID NO: 332)
```


AOLFR181 sequences:

MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIIKTEPSLHEPMYYFLAML
AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
IYGFFIALCTMLDLALIVLSYVLILKTILSIASLAERLKALNTCVSHICAVLTFYVMTTLAAMHHF
AKHKSPLVVILIADMFLLVPPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)


```
     ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCCTTCTGATTGGGATCCCAGGACTGG
 30  AACATGCCCACATTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGGC
     AACTGCACCATTCTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
     CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCTACCATGTTGA
     GGGTCTTCTTGTTCAATGCCATGGGAATTTCACCTAATGCCTGCTTTGCTCAAGAATTCTTC
 35  ATTCATGGATTCACTGTCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
     TGCCATTCACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
     GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTCCCTTCACCTTAAGGAG
     ATTAAAATATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
 40  AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
     TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAAATACCTGTGTCTCCCACATCTGTGCTGTG
     CTCACCTTCTATGTGCCCATCATCACCCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
     GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTTGGTGCCGCCCCTTATGAACCCC
     ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
 45  GTATGTGGGAGATAA (SEQ ID NO: 334)
```


AOLFR182 sequences:

MTLGSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIIKTERSLHEPMYLFL
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSSFLESSVLLSMAFDRFVAICHP
LHYVSILTNTVIGRIGLVSLGRSVALIFPLPFMLKRFPYCGSPVLSHSYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPIVYSVKTKQIRDRVTHAFCY (SEQ ID NO: 335)


```
     ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG
 55  GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
     GGTTTCCATCCCGGGCAACTGCACAATTCTTTTTATCATTAAAACAGAGCGCTCACTTCAT
```

GAACCTATGTATCTCTTCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
TCTCCCTACAGTCCTGGGCATCTTTTGGGTTGGGACGCAGAAATTAGCCATGATGCCTGC
TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTTCCTCGAGTCCTCTGTGCTACTGTCTATG
GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAGTGTAGCACTCATTTTTCCATTA
CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
TGTTTCCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCATCC
ATCGCTTTGGGAAAGCAGGCACCCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
CTTTCCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGATCCGGGATCGA
GTGACGCATGCCTTTTGTTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYYFL
SILALTDVSLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMAFDRFVAIRN
PLHYVSILTHDVIRKTGISVLTRAVCVVFPVPFLIKCLPFCHSNVLSHSYCLHQNMMRLACASTR
INSLYGLIVVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSTCLSHMSTVLLFYVPFMGA
ASMIHRFWEHLSPVVHMVMADIYLLLPPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCACCGTAACTTCATTCTGACAGGTATCCCAG
GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCCTGGGATTTCTCTACACACTCACACT
CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
ATGCTCAGCATCTACTGGTTTAATGCCCCTCAGATTGTTTTTGATGCATGCATCATGCAGAT
GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC
AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTCG
AAAGACTGGAATATCTGTCCTCACCCGGGCAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT
ATAAAGTGCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCATACTGTCTTCACCAAAA
CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTCACCCTGAAGAC
TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCTCAGCACCTGCCTCTCTCAC
ATGTCTACCGTGCTCCTCTTCTATGTTCCTTTTATGGGTGCTGCCCATGATCCACAGATT
TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

AOLFR184 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIIALQPALHR
PMHFFLFLLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFIHVFSVMESSVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSLFVVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
YIPMILLALINHPELPITQHHTHTLLSYVHFLLPPLINPILYSVKMKEIRKRILNRLQPRKVGGAQ
(SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCCTCATTGC
TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACTTCTTCCTCTTCTTGCTTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCCACACTGCTGGGCATCGCCCTTGCTGGTGCTCACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTTATCCATGTCTTTTCTGTCATGGAGTCCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGACTGGGTCTCCT
ATCTGCCCCTGCCATTCCTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCCTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTTGTGGTTCTTCAGCCATGGGTTTGGACCCCCTGCTTATTTTCTTCTTCCTAT

```
       GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
       CAAACCTGTGCTGCCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
       ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTCATGTCC
       ATTTCCTTCTTCCTCCATTGATAAACCCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
  5    AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGCTCAGTGA (SEQ ID NO:
       340)


       AOLFR185 sequences:

       MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTQSPWYPIVPSKSLVYNNNTCFDCYHLQR
  10   VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
       IDHTLHEPMYLFLAMLAITDLVLSSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
       MAMALDCYVATCFPLRHSSILTPSVVIKLGTIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
       EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
       SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPPMLNPIIYGVRTKQIGDRVIQGCCG
  15   NIP (SEQ ID NO: 341)


       ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCATGTT
       GTAACATATTATTTATTAAAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
       CTGGTATCCAATAGTCCCATCCAAAAGCCTTGTATATAATAATAACACTTGTTTTGATTGTT
  20   ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACCAGTCCATGGTGCT
       GGCTTCAGGGAACAGCTCTTCTCATCCTGGTGTCCTTCATCCTGGCTTGGAAATCCCAGGCCTG
       GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
       AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
       TTTCTGGCCATGCTGGCCATCACTGACCTGGTCCTCTCCTCCTCCACTCAACCTAAGATGTT
  25   GGCCATATTCTGGTTTCATGCTCATGAGATTCAGTACCATGCCTGCCTCATCCAGGTGTTCT
       TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGCTATGGCCCTGGACTGCTAC
       GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCGTGATCAAAC
       TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCTTCTGCTTCATGGTGTC
       TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
  30   CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
       CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT
       GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCTGTTGCTAATCTCTATCTACTGATACCTCCCATGCT
       TGTGTCATCTTGGCTCTTTATATCCCAGCCCTTTTTTCTTTCCTCACCTACCGCTTTGGCCAT
       GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
  35   CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGGACAGGGTTATCCAAGGATG
       TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)


       AOLFR186 sequences:

       MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
  40   FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
       RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
       NVMVIFVDIGVASGCFVLIVLSYVSIVCSILRIRTSDGRRRAFQTCASHCIVVLCFFVPCVVIYLR
       PGSMDAMDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLRDKVAHPQRK (SEQ ID NO:
       343)
  45

       ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCCAGGGC
       TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGGAACCT
       CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
       CCAACCTGTCCTTCATTGACATGTGGTTCTCACGGTCACGGTGCCCAAAATGCTGATGAC
  50   CTTGGTGTGCCCCAAGCGGCAGGGCTATCTCCTTCCACACAGCTGCGTGGCTCAGCTCTATTTTT
       TCCACTTCCTGGGGAGCACCGAGTGTTTCCTCTACACACGTCATGTCCTATGATCGCTACTTG
       GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
       CCACCGGCACCTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
       TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
  55   AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
       GGCCTCAGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATCGTCGTTCCATCCTGC
```

                              -160-

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
5   CCTCAGAGGAAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGILI
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHISFDGCLTQKFFIHFLFIHSA
10   VLLAMAFDRYVAICSPLRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

15   ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATGGCATGCGCCATCTACAT
20   GCAACTACATATCTGGCTGTCCATCTGCTGTAGCGTCGGTAGCATGGTCATGCGCCGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
GCCAATTTGTGGCTAGGTTATAGCCACATTTCCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATTCACTTCCTCTTCATTCACTCTGCTGTCCTGCTGGCCATGGCCTTGACCGCTATGTGG
CCATCTGCTCCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
25   CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
TCTGTCCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCCTACATCCACATCCTCCAAGCAGTCTTCCGC
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
30   TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTCATTCCTCCTATGCTCAAT
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

MFPSLCPCVLLVQLPLMNENMQCFVFCSCDSLLRMMVSRFIHVPFVKMKRIIVGGYSKHFFSN
35   ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRLRHLSPTPSEEHMKNKNNVTEFILL
GLTQNPEGQKVLFVTFLLIYMVTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRVCVL
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
40   AVITFTILLSYGVILHSLKTQSLEGKRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV
VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACTTATGAATGAGAACAT
GCAGTGTTTTGTTTTCTGTTCTTGTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
45   ATGTCCCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTTTGTAGGC
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTTATTTGTCACATT
50   CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
AGCCAGTCCCTGGGTCCCCCATGTACTTTTTTCTGGCTTCTTTATCATTCATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGCAGAAAAAGACCATTT
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGCTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGACATCTGTAAGCCTCTTCAAGCCTCTTCATGAATTGA
55   TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
ACAACTTCCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGCACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTCACCTTCTTCACTATCCTGC
TTTCCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAACGAAAAGC
TTTCTACACCTGTGCATCCCACGTCACTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT
GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
5   TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
GAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
(SEQ ID NO: 348)

10   **AOLFR189 sequences:**
MQQNNSVPEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSPMYFFLFYLSF
ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
TIMSQQVCIILVLAWIGSLIHSTAQIILALRLPFCGPYLIDHYCCDLQPLLKLACMDTYMINLLL
VSNSGAICSSSFMILISYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPMD
15   KMVAVFYTIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
GGCAGAAAATAGTGTTTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT
GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
TTTTATTTGTCCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
20   TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
CATTTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC
CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
GTTCTTGCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTTGAAAC
25   TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
CTCAAGTAGTTTCATGATTTTGATAATTTCATATATTGTCATCTTGCATTCACTGAGAAACC
ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGCACGTCTCACATAATTGTAGTCAT
CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCCGACCACTTTCCCCATGGACA
AGATGGTGGCAGTATTTTATACTATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT
30   GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:
MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
35   YAQTMPRRLCICLVLYSYTGGFVNAIILTSNTFTLDFCGDNVIDDFFCDVPPLVKLACSVRESYQ
AVLHFLLASNVISPTVLILASYLSIITTILRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPSSS
YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
40   GGATGCAACTGGGGCTCTTTGTGGTGTTCCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG
TAGCACCCTCATCGTGTTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTGTCA
TTGGAAATCTGTCATTTCTGGATCTCTGGATCTTCTCGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
45   ATCTCCAAGCCCCTGCTTTATGCTCAGAACATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
ATATTCCTATACTGGGGGTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCCTCTTACCTCTCCATCACCACCACCATCCTGAGGAT
50   CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACCATGCTCCTCCCCACCTGATCTCCGTTA
CCTTATACTATGGCTCCATTCTCTACAACTACTCCCGGCCAAGTTCCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCCATGTTGAATCCCATGATCTCA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

55

-162-

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
FIDVCYISSTVPKMLSNLLQEQQTITFVGCIIQYFIFSTMGLSESCLMTAMAYDRYAAICNPLLYS
SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV
5   MTAILTMFFGIASALVIMISYGYIGISIMKITSAKGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTCATCCTGCTGGGATTCTCAGATT
TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
10 TGGAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
CTTCCTCAGTAACCTGTCCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
TCTCCAACCTCTTACAGGAACAGCAAACTATCACTTTTGTTGGTTGTATTATTCAGTACTTT
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
ATGCTGCCATTTGTAACCCCCTGCTCTATTCATCCATCATGTCACCCACCCTCTGTGTTTGG
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
TAATCTTGTCCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTC
TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
20 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAGAGA
AAGTGCTGCTGA (SEQ ID NO: 354)

25 **AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMAYDRYAALCKPLHY
TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLLTLSCSDNYISEM
VIFFVVGFNDLFSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
CTGCAGATCCCAACTCTTCATAGTCTTCCTTTTCATCTACCTATTAGTGGGAAACCTTGGGA
35 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCCTCA
GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
GTTTCTCACAGGAGACAAATTCATATTTATATAATGCTTGTGCCACACAATTCTTCTTCTTTG
TAGCCTTTATCACTGCAGAAAGTTTCCTCCTGGCATCAATGGCTTATGACCGCTATGCAGC
ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGACT
CTCTCATGTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTGTGGTGGGATTCAATG
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG
TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACCTAACCTCAGCCATTTCATG
45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACGTAGGGAAGGCAA
AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

50 MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMAYDRYAAVCKPLHY
TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
55 357)

-163-

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
CTGCAGGTTCCCCTCTTTATAACGTTCCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
GGGAATTATTGTATTGATATTCTGGGATTCCTGTCTCCACAATCCCATGTACTTTTTTCTCA
GTAACTTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
AGCTTTTGGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACTGTGTGTGCTCGTCTGGCCA
TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGATGACCATTTAGTCTC
TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTTATTTATGTTGTGAGCTTCAATATCT
TTATAGCTCTCCTGGTTATCTTGATATCCTACACACATTCATTTTTATCACCATCCTAAAGATG
CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTCATTGCAGTCGG
CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA
TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
GTCGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNQSCVVEFILLGFSNYPELQGGQLFVAFLVIYLVTLIGNAIIVIVSLDQSLHVPMYLFLLNL
SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCFAQMYFILLFGGAECFLLGAMAYDRFAAICHPL
NYQMIMNKGVFMKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTFL
FEIYAFTGTFLIILVPFLLILLSYIRVLFAILKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLQ
PKSGYSPETKKVMSLSYSLLTPLLNLLIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
359)

ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCCTGGTTATTTATCCTGGTGACCCTGATAGG
AAATGCCATTATTATAGTCATCGTCTCCCTAGACAGAGCCTCCACGTTCCCATGTACCTGT
TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
GGTGGTCCTCTCTACTGAAAAAACTACAATTTCTTTTGGGACGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTTATGAAA
TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCCAGCAGTGT
TAGAACTTGCATGTGCAGACACGTTTTTGTTTGAAATCTATGCATTCACAGGCACCTTTTTG
ATTATTTTGGTTCCTTTCTTGTTGATACTCTTGTCTTACATTCGAGTTCTGTTTGCCCATCCTG
AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTCCACCTGTGCCGCTCACCTCACAT
CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
ACCGGAAACCAAGAAAGTGATGTCATTGTCTTACTCACTTCTGACACCACTGCTGAATCTG
CTTATCTACAGTTTGCGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVCFLAVNTFHVRSSFDFLKADDMGEINQTLVSEFLLLGLSGYPKIEIVYFALILVMY
LVILIGNGVLIIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVPSTLVSLISKKRNISFSGCAVQMFF
GFAMGSTECLLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSAVQTLLAMRL
PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVLPLMVIFFSYMFILYTILQMNSATG
RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR
NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

ATGATTGTTCAGTTAATTTGTACTGTTTGTTTCTTGGCAGTAAATACATTTCATGTTAGATC
TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTCAGAA
TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTTCTAATCATAGCCAGCATCTTTGATT
CTCATTTTCACACACCAATGTACTTCTTCCTGGGCAACCTCTCTTTCCTGGATATCTGCTAT
ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
TCTTGGCATGATGGCATTTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGGAATAA
ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
5   TCATTTCGCATGTGAAATATTAGCTGTCCTCCAAGCTGGCCTGTGCTGATATATCCCTCAATA
TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTGCATTTTTTC
TCCTATATGTTCATCCTCTACACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
10   AAGCTCATTTCTCTGTTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT
GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAAACCAATTCACTA
A (SEQ ID NO: 362)

15   AOLFR196 sequences:

MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLLVYTLTMVGNILLIILVNINSSLQIPMYYFLSNL
SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFASFADAECLILAAMAYDRYAAICNPLL
YTTLMSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLLALSCTDTQINQL
LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
YSLDTDKVVAVFYTVVFPMFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
20   ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTCACAGATTATC
TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAACTATGGTCGGA
AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATTCCCATGTATTATTT
25   TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTT
CTTCGCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
CAGCCATCTGCAACCCACTGCTCTATACTACACCTGATGTCTAGGAGAGTCTGTGTCTGCTT
30   CATTGTTGTTGGCATATTCAGTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGTATATCCCACCTCTTCT
GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG
AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
35   CAGTCACCTTATTCTATGGAGCGCTCCTGTTTTATGTGTTGTATTTCCCATGTTTAATCCAA
TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAGAATAGTCAATATCTAA (SEQ ID NO:
364)

40   AOLFR197 sequences:

MCYLSQLCLSLGEHTLHMGMVRHTNESNLAGFILLGFSDYPQLQKVLFVLILILYLLTILGNTTI
ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTLQLPFCGH
RQVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
45   GTCFSHLTVVTIFYGTIIFMYLQPAKSRSRDQGKFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
TGAGACATACCAATGAGAGCAACCTAGCAGGTTCATCCTTTTAGGGTTTTCTGATTATCC
50   TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
ATACCACCATCATTCTGGTTTCTCGTCTCGAGACCCCAAGCTTCATATGCCGATGTATTTCTTC
CTTTCTCATCTCTCCTTCCTGTACCGCTGCTTCACCAGCAGTGTTATTCCCCAGCTCCTGGT
AAACCTGTGGGAACCCATGAAAACTATCGCCTATGGTGGCCTTTTGGTTCACCTTTACAAC
TCCCATGCCCTGGGATCCACTGAGTGCGTCCTCTTGGCTCTGATGTCCTGTGACCGCTATGT
55   GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCCTGCA

-165-

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACCACGTTTAACGAGGCTGAGCTTTTGTGGCTAGTATCCTTT
TCCTTATAGTGCCTGTCTCATTCATCCTGGTCTCCTCTGGCTACATTGCCCACGCAGTGTTG
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTCGGGACCTGCTTCTCCCACCTGACA
5   GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
CCAGGGACCAGGGCAAGTTTGTTTCTCTTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10   **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFFVALATVENYLLASMAYDRYAAVCKP
LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
15   TSEVILVFMSSFNIFFVLLVIFISYLFIFITILKMHSAKGHQKALSTCASHFTAVSVFYGTVIFIYLQ
PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCCATGTACTTTTTCCTCAG
20   TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTCAGATGTTCTTCTTTGT
AGCCTTGGCCACGGTGGAAAATTACTTGTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC
25   TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
TTTTTGTTCTTCTAAGTTATCTTTATCTCCTACTTGTTCATATTCATCACCATCTTGAAGATGC
ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCCAGCTCCAGCCACTCCATGGAC
30   ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCTGTGGTCT
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAAT
TTCTATAA (SEQ ID NO: 368)

35   **AOLFR199 sequences:**

MDTGNKTLPQDFLLLGFPGSQTLQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
NLSFLEIWYTTAAVPKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLLAAMAYDRCLAICYP
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHFFCDIAPWIALACTNTQA
VELVAFVIAVVVILSSCLITFVSYVYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
40   TSIKDALDLIKAVHVLNTVVTPVLNPFIYTLRNKEVRETLLKKWKGK (SEQ ID NO: 369)

ATGGACACAGGCAACAAAACTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
45   TCTGAGCAACCTCTCCTTCCTGGAGATTTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
GCCATCCTACTGGGGAGAAGTCAGACCCATATCATTTACAAGCTGTCTTTTGCAGATGTACT
TTGTGTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
TGGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCCACCAGCCCTCATCAG
50   TGGCCTGTCTTCTGTGGCCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATTC
TCAGGATCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCCTTCACGTCCGCACCTCTATCAAAGAT
55   GCCTTGGATCTGATCAAAGCTGTCCACGTCCTGAACACTGTGGTGACTCCAGTTTTAAACC
CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVIYTLTVLGNLGMILLIRIDSQLHTPMYFFLANL
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
5   YSLIMSRTVYLKMAAGAFAAGLLNFMVNTSHVSSLSFCDSNVIHHFFCDSPPLFKLSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFSIFSMHSGEGRHRAFSTCASHLTAIILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
10   TGGAGCTACAGATTATCCTCTCTTTTTGTTTTTTCTTGTGATTTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACTCAACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTTGCTGGCTGCTTCCTACAGATGTACT
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCCTTTGGGTTAATGGCCTATGACAGGTA
15   TGCGGCCATATGTCGCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTTGCTGCAGGGTTGCTGAACTTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
TTCAAGCTCTCTTGTTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
20   TTTTCTATGCATTCGGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

25

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSIPSTLVSFLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
30   YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVVQLPFCRNNIINHFTCEILAVMKLACADISDN
EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDLDATDKIISMFYGVMTPMMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
373)

ATGGAATGGGAAAACCACACCATTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
35   CAAGACTTGAGTTACTCTTTTTTGTGCTCATTCTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGTCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCCT
CGGCTTGGCCATGGGGACAACAGATGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
40   GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGTCAAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTCACCTGTGAAATTCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC
45   TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCTCTACCTGTTCAGCCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSIPSTLVSFLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
55   YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVVQLPFCRNNIINHFTCEILAVMKLACADISGN
EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

-167-

ETLNSDDLDATDKLIFIFYRVMTPMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

ATGGAATGGGAAAACCACACCATTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCCT
CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTCACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCCTATTGACACCTTTGTTATTAATTATTGTCTTCTTACACGTTAATCATTTTGAGCATC
TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTCAGATGACTTGGATGCCACTCGACAAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

AOLFR203 sequences:

MKRQNQSCVVEFILLGFSNFPELQVQLFGVFLVTYVVTLMGNAITVIISLNQSLHVPMYLFLLN
LSVVEVSFSAVITPEMLVVLSTEKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLF
EIYAFTGTILIVMVPFLLILLSYIRVLFAILKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLIKLWRRKVILHTF (SEQ ID NO: 377)

ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAACTATGATTTCTTTTGTGGCGTGTTTTGCACGACATGTAT
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTTATGAAA
TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCGGTA
CTAGAGCTTGTGTGTGGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTTGATCCTCTTGTCTTACATTCGAGTTCTGTTTGCCATCCT
GAAGATGCCCATCACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

AOLFR204 sequences:

MEKKKNVTEFILIGLTQNPIMEKVTFVVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAWVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDTHTLGLFV
AVNSGFICLLNFLILVVSYVIILRSLKNNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSVTTLPI
DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTSDND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCATA
ATGGAGAAAGTCACGTTTGTAGTATTTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTATTTCTTCCTG
ACCCACCTTTCTTTGATAGACACCAGTTTATTCTTCTTCTTCAGCTCCTAAGTTGATTGTGGA
TTCCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT
GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG
CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAAA
5   ACTTGTTTGCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG
TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCCATTGAT
AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
10   TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAAGTGACTTCAG
ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL
15   DASYSFTVAPRMLVDFLSAKKIISYRGCITQLFFLHFLGGGEGLLLVVMAFDRYIAICRPLHYPT
VMNPRTCYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNSGLMTLLCFLGLLASYAVILCRIRGSSSEAKNKAMSTCITHIIVIFFMFGPGIFIYTRPFRA
FPADKVVSLFHTVIFPLLNPVIYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)

20   ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTTAATATTCTACTTCATCATCCTCCCTGG
AAATTTTCTCATTATTTTCACCATAAAGTCAGACCCTGGGCTCACAGCCCCCCTCTATTTCT
TTCTGGGCAACTTGGCCTTCCTGGATGCATCCTACTCCTTCACTGTGGCTCCCGGATGTTG
25   GTGGACTTCCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
TCTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTTGTGATGGCCTTTGACCGCTA
CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCCTAGAACCTGCTATGCA
ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCTCATCCT
CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACTTCTTCTGTGATGTCCCACAGGTC
30   ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTCGCATA
CGAGGGTCTTCTTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTG
TTATATTCTTCATGTTTGGACCTGGGCATTTTATCTACACACGGCCCTTCAGGGCTTTCCCA
GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCCTTTGTTGAATCCTGTCATTTA
35   TACCCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVFSVIYINAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI
DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGEHFFRGVEVILLTVMAYDHYVAICKPLHYT
40   TIMKQHVCSLLVGVSWVGGFLHATIQILFICQLPFCGPNVIDHFMCDLYTLINLACTNTHTLGLF
IAANSGFICLLNCLLLLVSCVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCIFVVMRPPATL
PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCSRKAISSVK (SEQ ID NO: 383)

ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
45   ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCATCTACATCAACGCCATGATAGGAAATG
TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTTCCTG
GCCTATCTCTCCTTTATTGATGCCTGCTATTCCTCTGTCAATACCCCTAAGCTGATCACAGA
TTCACTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
CATTTTTTCAGAGGTGTTGAGGTCATCCTACTTACTGTAATGGCCTATGACCACTATGTGG
50   CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT
GGGAGTGTCATGGGTAGGAGGCTTTCTTCATGCAACCATACAGATCCTCTTCATCTGTCAA
TTACCTTTCTGTGGTCCTAATGTCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA
TCTTGCCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTCATAT
GCCTGTTAAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTCATACTGTACTCCTTAAAGACC
55   CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTGTCTCCCACATCACAGTTGTCA
TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5   **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISMTGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP
10   ESKASVDSGNEDIIEALISLFYGVMTPMLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCCTGGTAGGGCTTTCTGCCCACC
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA
15   AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGTATTTCTT
CCTCTGTAATCTTTCCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20   TGGCAGCTGGGTCCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTAGTGACAGGGTCGAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA
25   GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30   **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYLFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSINHFTCEILAILKLVCVDTS
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
35   LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTTCTTCCTGGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40   AACATTTTTCTGATCTCCATCAACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAACTTTGTTTCAGGGAGAAACACTATTTCATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45   TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCCACCTGA
50   TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAAATAGACAAATTGATAAGTTTGGTGTATGCCGGACAAACCCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFFALILVMYVVILIGNGVLIIASILDSRLHMPMYFFLGNLS
FLDICYTTSSIPSTLVSLISKKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY
PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPFCGNNIINHFLCEILAVLKLACSDISVNIV
TLAVSNIAFLVLPLLVIFFSYMFILYTILRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
389)

ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
CCAAACTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
CCTGGGCAACCTCTCTTTCCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
TGAGCTTAATCTCAAAGAAAAGAAACATTTCCTTCTCTGGATGTGCAGTGCAGATGTTCTT
TGGGTTTGCAATGGGGTCAACAGAATGTTTCCTCCTTGGCATGATGGCATTTGATCGTTAT
GTGGCCATCTGTAACCCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
TGACTTCTGTATCATGGCTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT
GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
TAAAATTAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
TTCCTAGTTCTTCCTCTGCTCGTGATTTTTTTCTCCTATATGTTCATCCTCTACACCATCTTG
CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTCTACATGCCAGCTCACCTGACTG
TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
CTTGGGAAAGACAACTTGCAAGCTACAGAGGGGCTTGTTCCATGTTTTATGGGGTTGTGA
CCCCCATGTTAAACCCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRRNDTNVADFILTGLSDSEEVQMALFMLFLLIYLITMLGNVGMLLIIRLDLQLHTPMYFFL
THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCFAQMFCFVFLGTAECYLLSSMAYDRYAAICSP
LHYTVMPKRLCLALITGPYVIGFMDSFVNVVSMSRLHFCDTSPILALSCTDTDN
TEMLIFIIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTMIFTYLKP
RKSYSLGRDQVAPVFYTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCCATGTAT
TTTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAAC
CTTAGCGAACTTACTGACTTCCAACTATATTTCCTTCACGGGCTGCTTTGCCCAGATGTTCT
GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
GCAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGCCCAAAAGGCTCTGCCTCGCTC
TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTTCTGTGACACTTCCCCAATTTT
AGCTCTGTCCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC
ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
GGAGTCACCATCTTCTATGGAACTATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

AOLFR211 sequences:

MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILIIRLDLQLHTPMYFFL
THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCFAQMFFFAFLGTAECYLLSSMAHDRYAAICSP
LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMSRLHFYDSNVIHHFFCDTSPILALSCTDTYNT
EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLKPRK
SYSLGRDQVASVFYTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
GGGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
5   TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
TTAGCGAACTTACTGACTTCCAACTATATTTCCTTTACGGGCTGCTTTGCCCAGATGTTCTT
TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG
CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
10   GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
GCTCTGTCCTGCACTGATACATACAACACCGAAATCCTGATATTCATTATTGTTGGTTCCAC
CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTCATTCTCTTTACCATCCTGA
AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTGGG
AGTCACCATCTTTTATAGCACTCTGATTTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT
15   TGGGAAGAGATCAAGTGGCTTCTGTTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT
CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20   MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFTVLGNLGLITLIRMDSQLHTPMYFFLSN
LAFIDIFYSSTVTPKALVNFQSNRRSISFVGCFVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
LYSVVMSQKVSNWLGVMPYVIGFTSSLISVWVISSLAFCDSSINHFFCDTTALLALSCVDTFGT
EMVSFVLAGFTLLSSLLIITVTYIIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
25   NTSSLTQAQVASVFYTIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAATCACC
CTGAATTACAAGTCAGTCTTTCTTGATGTTCTCTTCATTTATCTATTCACTGTTTTGGGA
AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
30   TCCTGAGCAATTTAGCATTTATTGACATATTTACTCCTCTACTGTAACACCTAAGGCATTG
GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTCCAAATGTACTT
TTTTGTTGGATTGGTGTGTTGTGAGTGTTTCCTTCTGGGATCAATGGCCTACAATCGCTACA
TAGCAACTGCAATCCCTTACTGTATTCAGTAGTCATGTCCCAAAAAGTGTCCAACTGGCT
GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
35   AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTTGTGACACCACAGCTCTTTTAGC
ACTCTCCTGTGTAGATACATTCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG
GATCCAGTCAGCAGCAGGCAGGCAGACAGAAGGCCTTCTCCACCTGCGCATCCCACTCATGGCT
GTAACTATCTTTTATGGGTCTCTGATTTTCACCTATTTGCAACCTGATAACACATCATCGCT
40   GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCATTCCCATGCTGAATCCACTC
ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45   MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDHPRL
EAVLFVFVLFFYLLTLVGNFTIIIISYLDPPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVIMNPRLCQQLASISWLSGLA
SSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVVSVLFVVIPPALISISYGFI
TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVTPTLNP
50   IIYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
ATTTAATTGTTTTGGATGTACCCATTCCATTCCTGCCTTAGGTGCGGATCCCCCTGGAGGG
ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTCATCCTTCTAGGCTTCTCAGACCACC
CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCCTTTTCTTCTACCTCCTGACCCTTGTGGGA
55   AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTTT
TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

-172-

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCCTAATCCATGCAACTTTTACCTTG
5   CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGATGGTGCTTTTTGTTGATTGTTCTGT
TTGTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCCACCTTACAG
TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
10   CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGGGA
AAATTGTGA (SEQ ID NO: 398)

15   **AOLFR214 sequences:**

MDKSNSSVVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
YVVIMSRRTCTVLVMISWAVSLVHTLSQLSFTVNLPFCGPNVVDSFFCDLPRVTKLACLDSYIIE
ILIVVNSGILSLSTFSLLVSSYIIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFIYVWPFTIS
PLDKFLAIFYTVFTPVLNPIIYTLRNRDMKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
20   NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
AAAAACTCCAGCTTTTCTATTTTTGTTTCTTCTCTGTGTTGTATACAGTCATTGTGCTGGGA
AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
25   CTTGGGAAACCTTTCCTTTGTTGACATTTGTCAGGCTTCTTTTGCTACCCCTAAAGATGATTG
CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTTT
ATTCACCTTTTTACTGGAGGGGAGATGGTGCTACTTGTTTCGATGGCCTATGACAGGTATG
TAGCCATATGCAAACCCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
GGTAATGATCTCCTGGGCTGTGAGCTTGGTGCACACATTAAGCCAGTTATCATTTACTGTG
30   AACCTGCCTTTGTGGACCTAATGTAGTAGACAGCTTTTTTTGTAGACTTCTTCCTCGAGTCAC
CAAACTTGCCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT
CTTTCCCTAAGCACTTTCTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTTACAGTTTG
GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
GTAATATTATTCTTTGGACCTTGCATCTTCATCTATGTGTGGCCCTTTACCATCTCTCCTTT
35   GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCCGTCCTAAACCCCATTATTTATA
CACTAAGGAATAGGGATATGAAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
400)

40   **AOLFR215 sequences:**

MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVIISFDSHLNSPMYFLLSNL
SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
YSTIMNRRLCVIFVSISWAVGVLHSVSHLAFTVDLPFCGPNEVDSFFCDLPLVIELACMDTYEM
EIMTLTNSGLISLSCFLALIISYTIILIGVRCRSSSGSSSKALSTLTAHITVVILFFGPCIYFYIWPFSRL
45   PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
AATGTCTTAATTATTGTCATTATTTCTTTTGACTCCCATTTGAACTCTCCTATGTACTTTCTG
50   CTCAGTAATCTTTCTTTCATTGATATCTGTCAGTCTAACTTTGCACACCCCCAAGATGCTTGT
AGACTTTTTTATTGAGCGCAAGACTATCTCTTTGAGGGTTGCATGGCCCAGATATTCGTT
CTTCACAGTTTGTTGGGAGTGAGATGATGTTGCTGTTAGCTATGGCATATGACAGATTTA
TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
TGTGTCTATTTCCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG
55   ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

-173-

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCCTACACCATCATTTTGATCGGTGTCCG
ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACACATTAACTGCCCACATCACAGTG
GTCATTCTTTTCTTCGGGCCTTGCATTTATTTCTATATATGGCCTTTTTAGCAGACTTCCTGT
GGACAAATTTCTTTCTGTCGTTGTTCTACACTGTTTGTACTCCCTTGTTGAACCCCATCATCTACT
5   CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCCATCATGTGAACT
CCTGGAAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMYFLL
10   TNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPL
HYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCDLPVVFQLACVDTY
VLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
PLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRKLKNRFLNFNKAMPS (SEQ ID NO: 403)

15   ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
GGGAACTACAGATGTTTTTCTTTATGGTGTTTTCATTGCTTTATGTGGCAACAATGGTGGG
TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTCGCCACCCCAAAGATGATT
ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
20   TTCTCCACCTTTTCACTGGAACTGAGATCATCTTACTCATGGCCATGTCCTTTGATAGGTAT
ATTGCAAATATGCAAGCCCCTGCACTATGGCTTCTGTCATTAGTCCCCAGTGTGTGTTGCTCT
CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
ACGTTACCATTCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCCTGTGGTGTT
CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGGCCTCTTTATGATCTCAACAAGTGGCATA
25   ATTGCGTTGTCCTGTTTTATTGTTTTATTTAATTCATATGTTATTGTCCTGGTTACTGTGAA
GCATCATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTCATTGTTG
TCTTCTTGTTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT
30   TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISFEGCMTQMFFLHLLGGAEIVLLISMSFD
35   RYVAICKPLHYLTIMSRRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSFFCDLPLVIK
LACVDTYILGVFMISTSGMIALVCFILLVISYTIILVTVRQRSSGGSSKALSTCSAHFTVVTLFFGP
CTFIYVWPFTNFPIDKVLSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
(SEQ ID NO: 405)

40   ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTGCACCATTGCATCA
GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
CCTGGCCTCAGTTTGCCACCCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
45   TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCCTACATCTCTTAGGGGGTGCTGAGATTG
TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATTACTTTCCTGGATTGTCGGCATCT
TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGCTGTCGACACATATATTC
50   TGGGGGTGTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTCTGGT
GATCTCTTACACTATCATCCTGGTCACCGTTCGGCAGCGTTCCTCTGGTGGTCAACCTCCAAA
GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCTTTTCTTTGGCCCATGCACTTT
CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
55   CATGAGGAAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
(SEQ ID NO: 406)

-174-

AOLFR218 sequences:

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNILIICTIRLDPHLTSPMYFLLANLA
LLDIWYSSITAPKMLIDFFVERKIISFGGCIAQLFFLHFVGASEMFLLIVMAYDRYAAICRPLHYA
TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVVLMFGPSIYIYARPFD
SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
GGGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTCATCCTACCAGGA
AATATCCTTATCATTTGCACCATCAGGCTAGACCCTCATCTGACTTCTCCTATGTATTTCCT
GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTAAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCCTTTGGTGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCATTCTATAATACAGGTGGCTCTCATTGTT
CGACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG
TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGCTCA
AGAAACATTCAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT
TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCCTTTACTTAATCCCATT
ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
ATTTTGTGTGAAGAAGTGA (SEQ ID NO: 408).

AOLFR219 sequences:

MLTSLTDLCFSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF
LIILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWFVGFIHTTSQLAFTVNLPFCGPN
KVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVRNRSSASMAKAR
STLTAHITVVTLFFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS
RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409)

ATGCTCACTTCATTAACTGATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
AGATTTTCTTTGTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
GTGTTGTGCTGGTCCTCATTTCATGGTTTGTGGGCTTCATCCATACTACGAGTCAGTTGGCA
TTCACTGTTAATCTGCCATTTTGTGGTCCTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC
TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT
AGTGGCTTTCTTTCTCTGAGTTCCTTTCTCCTCTTGGTTGTCCTCACACTGTAATACTTGTT
ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGT
AATCTACACGCTAAGAAACAAAGAAGTGAAGGCAGCTATGTCAAAACTGAAGAGTCGGTA
TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCCTAGAAACAAAGTAA
(SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG
FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
HSLGITESCVLTAMAIDRYIAICNPLRYPTIMIPKLCIQLTVGSCFCGFLLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAHLAVFLLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5   ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
    GTGTTCACAGATGACACAGTTGACGGCCAATGGGACATCAGACAATGGTGACTGAGTTCCT
    CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
    TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCATTGTCATCCAGGTGGGCATGGC
    CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCCTCTCCTTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCCTGCCTAATCAGTGAGCAGAAGAGCATTCCGTGGC
    TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCCTG
    ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
    TGATTCCCAAACTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTTGGCTTCCTCCTTGTG
    CTTCCTGAGATTGCATGGATTTCCACCTTGCCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTCTGTGATTTCACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCCTAGTGGTTCATT
    GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA
    TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC
    CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTGGCAGTGTGGCTGTCATGTATT
    TGAGATTCTCAGCCACCTACTCAGTGTTTGGGACACAGCAATTGCTGTCACTTTTGTTATC
20 CTTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
    TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
    412).

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFFAIYLLTLLENALIVFTIWLAPSLHRPMYFFLGH
    LSFLELWYINVTIPRLLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
    LLYPSLMPSSLATRLAAASWGSGFFSSMMKLLFISQLSYCGPNIINHFFCDISPLLNLTCSDKEQA
    ELVDFLLALVMILLPLLAVVSSYTAIIAAILRIPTSRGRHKAFSTCAAHLAVVVIYYSSTLFTYAR
    PRAMYTFNHNKIISVLYTIIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

    ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
    CTCCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA
    ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTC
35 CTTGGCCATCTCTCTTTCCTGGAGCTATGGTACATCAATGTGGGCTGTATGACCCAACTGTACTTC
    TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
    GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
    CTGCTGCCTCTGGGCCAGTGGCTTCTTCAGCTTCTTGGAAGCTTCTTTTTATTTCCCAA
40 TTGTCCTACTGTGGACCCAACATTATCAACCACTTTTTCTGTGATATTTCCCCACTACTCAA
    CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
    ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
    GATCCCTACGTCCAGGGGACGGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
45 GTTGTTATCTACTACTACTCCTCCACTCTCTTCACCTATGCACGGCCCCGGGCCCATGTACACCTT
    CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
    TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
    GTCACTATCCTAGGGATGTTCAGGACTGA (SEQ ID NO: 414).

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLTSNVFIIIAIRLDSHLHTPMYLFLSFL
    SFSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
    HYASHMNPTLCAQLVITSFLTGYLFGLGMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
    ELRIFILSLLVLLVSFFFITISYAYILAAILRIPSAEGQKKAFSTCASHLTVVIIHYGCASFVYLRPK
    ASYSLERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

-176-

```
ATGGGGCAGACCAACGTAACCTCCTGGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCCTCTCTCTGTATCTAGTCACTCTGACCAGC
AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCCATGTACCTCTT
CCTTTCCTTCCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCCAGATGTTCTT
TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCCAGCT
GGTCATTACTTCCTTCCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC
ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCCTTTATCCTCAGTCTTTTGG
TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
AGGATCCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
TGGTCATTATTCATTATGGCTGTGCTTCCTTCCTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).
```

AOLFR223 sequences:

```
MEAANESSEGISFVLLGLTTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
HPLPYATRMSRAMCAALVGMAWLVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLLRLSC
SDTHHIQLLIFTEGAAVVVTPFLLILASYGAIAAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT
VIAVYFQATSRREAEWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
(SEQ ID NO: 417).
```

```
ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA
GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGCTCTTGTATGTGGCCAGCCTCCTG
GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
TCCTGCTGGCCCACCTGTCCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCCAAGATG
TTGGCCAACTTGTTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGGCTGACCCAAATGT
ACTTCTTCTTTGCCCTGGGGGTAACTGATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
CTACGTGGCCATCCGGCACCCCCTCCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
GCCCTGGTGGGAATGGCATGGCTGGTGTCCCACGTCCACTCCCTCCTGTATATCCTGCTCA
TGGCTCGCTTGTCCTTCTGTGCTTCCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT
CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG
CCGCAGTGGTGGTCACTCCCTTCCTGCTCATCCTCGCCTCCTATGGGGCCATCGCAGCTGC
CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCATGTACACTGTAGTCACCCCCCATGC
TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGGCACTCCGAGCCCTTCT
CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).
```

AOLFR224 sequences:

```
MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTLFGNTIIIALSWLDLRLHTPMYFFLSHLSL
LDLCFTTSTVPQLLINLCGVDRTITRGGCVAQLFIYLALGSTECVLLVVMAFDRYAAVCRPLHY
MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTCGSHLLVVFLFYGSAIYT
YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:
419).
```

```
ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTTATTTTCTACTCCCTAACTCTCTTTGGC
AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTTT
TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCACCACCAGCACCGTGCCCCAGCTCCTGA
TCAACCTTTGCGGGGTGGACCGCACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT
```

```
GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCT
GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG
GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGACCTGTATTTCTGAA
GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT
CGTGGCTGTTCCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
GTAGTTTTCCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTATACTATAATTACCCCCATTCTCAATCCTC
TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
GCAGGGACTCAGGGTAG (SEQ ID NO: 420).
```

AOLFR225 sequences:

```
MENYNQTSTDFILLGLFPPSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLLASMAYDRYIAICFPLHYLIRM
SKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
FLSATIFLVFPFIGISCSYGQVLFAVYHMKSABGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).
```

```
ATGGAAAATTACAATCAAACATCAACTGATTTCATCTTATTGGGGCTGTTTCCACCATCAA
TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTCATTTTCCTGATGGCTCTAATTGGAAACC
TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCCTACTG
AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTGTTCCTAAGATGGCATCTGA
TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGAGTTTCTTCTTCT
TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
TATTTGCTTTCCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
TCGTGTTTCCCTTCATTGGTATTTCATGTTCCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
ATGAAATCTGCAGAAGGGAGGAAGAAAGACCTATTTGACCTGCAGCACCCACCTCACTGTA
GTAACTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
AACAGAGGACAAGGTTCTGGCTGTCTTCTACAACCATCCTCACCCCAATGCTCAACCCCATC
ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).
```

AOLFR226 sequences:

```
MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
ANMSFLEIWYVTVTIPKMLAGFVGSKQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
RYMAICYPLHYPVVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISSAAGRYKAFSTCASHLTVVIIF
YAASIFIYARPKALSAFDTNKLVSVLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQDPDP
KKASRNV (SEQ ID NO: 423).
```

```
ATGGAGTGGCGGAACCCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGCTGCTGGCCTATGTGTTGGTGCTGAC
TGAGAACACACTCATCATTATGGCCAATTAGGAACCATTCTACCCTCCACAAACCCATGTAC
TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
ATGACACAGCTCTACTTTTTCCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT
GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCAGTGGCC
GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA
AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTC
ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTGACTGGCGCCTATAAGGCCTTTTCCACCTGT
TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC
```

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:
MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFLMHRGLCARLVVVSWCTGVSTGFLHSMMISRLDFCGRNQINHFFCDLPPLMQLSCSRV
10 YITEVTIFILSIAVLCICFFLTLGPYVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMYV
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCATTTTCCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCTTCTCCTA
GCCAACCTGCTGTCCTGGGGCCAAGCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT
TCTTCGTATTCCTCGGCGGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACGGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTCAGCACAGGCTTTCTGCATTCCATGATGATTTCC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTCATTGTGTCCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTCCACATGTGGCTCCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:
MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHIDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAAWLGGSIDGFLLTPVTMQFPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQK
VVGRCVSSGKVTTF (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACTTTATCATATCTCTTTCGTGTACCCTACAGA
40 GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCTTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCCTTTGCTGGATGCACTGCCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCCTCCTAGGACTCATGTCCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCA
TGCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTA
50 TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCACTCATTTACAGCCTTAGGAACAAGGATGTCACGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMDSRLHTPMYFLLS
QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP
LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSCTDTS
LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSVFYGAAFY
TNVLPHSYHTPEKDKVVSAFYTILTPMLNPLIYSLRNKDVAAALRKVLGRCGSSQSIRVATVIR
KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCTT
CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCCTGCTGGGTCTCATGGCCTATGACCGC
TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACGCCAGGGTTTGCTTATT
CATGGTGGTCGGCTCCTGGGTTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
GCTGAAGTTGTCTTGCACAGACACGTCACTCTATGAGACCCTGATGTATGCCTGCTGCGTG
CTGATGCTGCTTATCCCTCTATCTGTCATCTCTGTCCTACACGCACATCTCCTGACTGT
CCACAGGATGAACTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCCTCCCACATT
ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
ACACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCAATCTCACCCCCATGCTCAA
CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
GAGATGTGGTTCCTCCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
NO: 430).

AOLFR231 sequences:

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSLLHTPMYFLLSNL
SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP
LHYMTIMSPRVLTGLLLSSYAVGFVHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
LQLLVIADSGLLSLVCFLLLLVSYGVIIFSVRYRAASRSSKAFSTLSAHITVVTLFFAPCVFIYVW
PFSRYSVDKILSVFYTIFTPLLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTTGTTGGGACTTTCCAAATCTC
AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
AACCTGCTCATCTTGGTGACTGTGACCTTTGATTCGCTCCTTCACACACCAATGTATTTTCT
GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG
TAGATTTCCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCCAGATGTTCTT
TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCCACGGGTGCTCACTGGGC
TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG
ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCCTTGTGAT
TAAACTTGCCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
CTGTCACTGGTCTGCTTCCTCCTCTTGCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
GATAAAATTCTTTCTGTGTTTTACACAATTTTCACACCTCTCTTAAATCCTATTATTTATAC
ATTAAGAAATCAAGAGGTAAAAGCAGCCATTAAAAAAAAGACTCTGCATATAA (SEQ ID NO:
432).

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
VIFVVFLMALSGNAVLILLIHCDAHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVNKIS
APBCGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
GFTFTPITMTFPFRGSREIHHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMLLIPVVIISSSYLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTILTPVVNP
LIYSLRNKDVMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

```
     ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTCATCCTGATGGGAC
  5  TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
     GTCGGATTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
     GTCATTTTTGTGGTTTTCCTGATGGCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACA
     CTGTGACGGCCCACCTCCACACCCCCATGTACTTTTTCATCAGTCAATTGTCTCTCATGGACA
     TGGCGTACATTTCTGTCACTGTGCCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
 10  GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTCAGAA
     TTTTTCCTTCTAGCCACCATGGCCTATGACCGGCTACGTGGCCCATCTGCCATCCTCTCCGTTA
     CCCTGTCCTCATGAACCATAGGGTGTGTCTCTTCCTGTCATCAGGCTGCTGGTTCCTGGGCT
     CAGTGGATGGCTTCACATTCACTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA
     GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
 15  TCTATGAGATTTTCATGTACTTGTGCTGTGTCCTCATGCTCCTCATCCCTGTGGTGATCATT
     TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA
     AAAAGGCCTTTGCCACCTGCTCCTCCCACTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
     ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCTGAGAAGGACATGATGGTATCTG
     TCTTCTATACCATCCTCACTCCAGTGGTGAACCCTTTAATCTATAGTCTTAGGAATAAGGAT
 20  GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG
     TAG (SEQ ID NO: 434).
```

AOLFR233 sequences:

```
25  MANITRMANHTGKLDFILMGLFRRSKHPALLSVVIFVVFLKALSGNAVLILLIHCDAHLHSPMY
    FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
    YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI
    LSCSDTSLYETLMYLCCVLMLLIPVTIISSSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
    GAAVYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLTVRFVL
    (SEQ ID NO: 435).
30
```

```
    ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTCATCCTCATGGGAC
    TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCCTGAAG
    GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACACTGTGACGCCCACCTCCACAGCC
35  CCATGTACTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
    CCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
    ATGCAGATGTTCCTCTATCTGACACTAGCAGGTTCGGAATTTTTCCTTCTAGCCACCATGGC
    CTATGACCGCTACGTGGCCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
40  GTCGTGTCTTTTCCTGGCATCGGGCTGCTGGTTCCTGGGCTCAGTGGATGGCTTCATGCTCAC
    TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
    TCCCTGCTGTAACGATCCTGTCCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA
    TGCTGTGTCCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT
    CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGAAAAAGGCCTTTGCCACCTGCTC
45  CTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCCC
    GGTGCTGAACCCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
    ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).
```

AOLFR234 sequences:

```
    MPNSTVVMEFLLMRFSDVWTLQILHSASFFMLYLVTLMGNILIVTVTTCDSSLHMPMYFFLRN
50  LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVVFFVYVELLFLTIMAHDRYVAVCQPL
    HYPVIVNSRICIQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE
    VMIVVSALGVGGGCFIFURSYHIFSTVLGFPRGADRTKAFSTCIPHILVVSVFLSSCSSVYLRPP
    AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).
```

```
55  ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
    TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC
```

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
5   TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACTCTCGAATCTGCATCCAGATGACACT
GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
CCCTTCTGTCGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTCACATCTTTTCGACCGTGCTCGGGTT
10   TCCAAGAGGAGCAGACAGAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCCTATTATTTA
CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIAILFSYLLTLLGNSTIILLSRLEARLHTPMYFFLSNL
SSLDLAFATSSVPQMLINLWGPGKTISYGGCITQLYVFLWLGATECILLVVMAFDRYVAVCRPL
RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
20   NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVVFLFYGSASYGY
LLPAKNSKQDQGKFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLLGKGREVG (SEQ ID NO:
439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
25   CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCTCCTATTTGCTGACCCTACTTGGG
AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
CTTCCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTTGACCGCTAC
30   GTGGCAGTGTGCCGGCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC
TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
GCAGCTCCCATTGTGTGGGCACCGGAGGGTGGAGGGATTCCTCTGCGAGGTGCCTGCCAT
GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
35   GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGGCCAAGAAC
AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA
ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTVPKVMAGLLTLDGKVIS
FEGCAVQLYCFHFLASTECFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
45   AAIHTSLTFRLLYCGPCHIAYFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
AVLRIRTAQGRQRAFSPCTAQLTGVLLYYVPPVCIYLQPRSSEAGAGAPAVFYTIVTPMLNPFIY
TLRNKEVKHALQRLLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
50   GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
CTGTGGTGAGCCACTTCTTCCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
CTTCCTCCTCTTCCTCCTCATCTACAGCATCACTGTGGCTGGAAATCTCCTCATCCTCCTAA
CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCCTGGGGCACCTCTCCTTC
CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
55   ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
CAGCACTGAGTGCTTCCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

-182-

```
       CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
       TGGGCCATAGGTGGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
       GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCTGTCCTAAAGCTCGGCCTGT
  5    ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
       GCCTCATCCTCATCGTTATTTCCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
       GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCCAGCTCACTGGGGTGCTCCTGT
       ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
       CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCATTTACACTTTGCGGA
       ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 10    CAGGCAGCCCACCCCCATAG (SEQ ID NO: 442).


       AOLFR237 sequences:
       MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
       RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRYIAISKPL
 15    HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLLPLPVCGPNVLDTFYCDVPQVLKLACTDTFT
       LELLMISNNGLVSWFVFFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVVTLHFVPCIYVYA
       RPFTALPTDTAISVTFTVISPLLNPIIYTLRNQEMKLAMRKLKRRLGQSERILIQ (SEQ ID NO:
       443).


 20    ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
       GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
       AAACTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
       TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCCTCCATCACAGCTCCTAAGGTCCTG
 25    ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
       TCTTCCACCTTCTGGGGGGAGCAGGATTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT
       ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
       TCATCGTGGGCTTCCTGGGTGGGGGGCTTGTCCACTCCATAGCGCAGATTTCTCTATTGCT
       CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC
 30    TCAAACTTGCCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
       AGTCAGTTGGTTTGTATTCTTCTTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
       GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACCG
       TGGTGACCCTGCATTTCGTGCCCTGCATCTATGTCTATGCCCGGCCTTTCACTGCCCTCCCC
       ACAGACACTGCCATCTCTGTCACCTTCACTGTCATCTCCCCTTTGCTCAATCCTATAATTTA
 35    CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
       AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).


       AOLFR238 sequences:
       MAPENFTRVTEFILTGVSSCPELQIPLFLVFLVLYVLTMAGNLGIITLTSVDSRLQTPMYFFLRHL
       AIINLGNSTVIAPKMLMNFLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40    LLYMVVVSRRLCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFYCDIAPLLALSCSDTYIPE
       TIVFISAATNLFFSMITVLVSYFNIVLSILRIRSPEGRRKAFSTCASHMIAVTVFYGTMLFMYLQP
       QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
       445).


 45    ATGGCTCCTGAAAATTTCACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
       CAGAGCTCCAGATTCCCCTCTTCCTGGTCTTCCTAGTGCTCTATGTGCTGACCATGGCAGG
       GAACCTGGGCATCATCACCCTCACCAGTGTTGACTCTCGACTTCAAACCCCCATGTACTTTT
       TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCATTGCCCCTAAAATGCTG
       ATGAACTTTTTAGTAAAGAAGAAAACTACCTCATTCTATGAATGTGCCACCCAACTGGGAG
 50    GGTTCTTGTTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
       TGTGGCCATTTGTAACCCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC
       TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACCTTGTATATTC
       TCTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTACTGTGATATTGCACCTCTGTT
       AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55    AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTGTCCATTCTA
       AGGATACGTTCACCAGAAGGAAGGAAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA
```

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACTGATAAGATGGCTTCTGTGTTTACACATTGGTGATTCCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMAQIFFLHFTGGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASWVVGFVHSISQVAFTVNLPYCGPNEVDSFFCDLPLVIKLACM
DTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRVTFQ (SEQ ID NO: 447).

10

ATGGACCCACAGAACTATTCCTTGGTGTCAGAATTTGTGTTGCATGGACTCTGCACTTCAC
GACATCTTCAAAATTTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCCATTATGCTGGGT
AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
CCTGCTGGGGAACCTAGCTTTCCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
ATCAGGGATTTCCTTAGTGATCAAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
TCTTCTTGCATCTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCCTTGCATTACATGACTTTGATGAGTTGGCAGACTTGCATC
AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
GTGATCAAACTTGCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
TGGTAGTGACGCTGTTCTTTGGCCCTTGCATTTTTGTTTATGTGCGGCCTTTCATGAGGTTC
TCTGTGGACAAGCTGCTGTCTGTGTTTATACCATTTTTACTCCACTCCTGAACCCCATTAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAAACTGCAAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLANLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLFFGTASITYIRPQ
AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRALRHLVKRQRPSP (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACACCACTGACATCGTGCCCAGGACCCT
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTTCCAGGGCTGTGCAGCCCAGATG
TACGTCTTCATTGTCCTGGGCATCTCGGAGTGCTGCCTGCTCACCGCCATGGCCTATGACC
GATATGTTGCCATCTGCCAGCCCCTACGCTATTCCACCCTCTTGAGCCCACGGGCCTGCTT
GGCCATGGTGGGGTCCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
ATCTTCTCTCTACCTTTTCGCCAGCCACCCGATCATCCCGCACCTTTCTCTGTGACATCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATCCCCTTCTCTCTGTATTGTCACCTCTTACATCCGCATCCTGGGTG
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
TCTGCTCGTGGTCTCTCTCTTCTTTGGAACAGCCAGCATCACCTACATCCGGCCGCAGGCA
GGCTCCTCTGTTACCACAGACCGCGTCCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCCTCACCCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55 MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLLGFSSLGEIQLALFVVFLFLYLVILSGNVTIIS
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

-184-

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTILKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYTIVTPLLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTTCTTTTCTGTATCTAGTCATTCTTAGTGGCAA
TGTCACCATTATCAGTGTCATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTTATGATCGCTATGCTG
CCATTGTCACCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTAGTTTTCAGCC
TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCATTTGTGGAGTTCTTGTAC
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTCATTATGGCTGTGCTTCCTTCATCTACCTGAGGCCTACAGCAAACTATGTGTCC
AACAAAGACAGGCTGGTGACGGTGACATACACGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACTTGCTATCAGAAAAGTGTTGGGCAAGAAA
GGTTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25

MNTTLFHPYSFLLLGIPGLESMHLWVGFPFFAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIFLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGIARLSCASIRVNIIYG
LCAISILVFDIIAIVISYVQILCAVFLLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFGR
NIPHFIHILLANFYVVIPPALNSVIYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTCATCCTTACTCTTTCCTTCTTCTGGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCCTTTCTTTGCTGTGTTCCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTCAGACTGACAGTAGTCTCCATCATCCTCATGTTCTACTTCCTG
GCCATTCTGTCATCTATTGACCCGGGCCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAGTTATGGCA
CTGGCCATCTTTCTGAGACCCTTAGTCTTTGTCATACCCTTTGTTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC
CTGTCTTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCATTTCCTATGTGACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTCAGCACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTTCTCATTCATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
ATTTATGGTGTCAGAACCAAACAGATTAGAGCACAAGTGCTGAAAATGTTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50

MEQVNKTVVREFVVLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGRGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLASQHSGF
SQLVIFMLGVFALVIPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSCASFIYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRTIGQTFYPLS (SEQ ID NO: 455).

55

ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC

```
          AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
          CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG
          TTGACCTGCTGTCCCAGAAGAAGAACCATTTCTTTCCTGGGCTGTGCCATCCAAATGTTTTCC
          TTCCTCTTCTTGGCTCCTCTCACTCCTTCCTGCTGGCAGCCATGGGCTATGATCGCTATAT
     5    GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
          ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
          TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCCTTA
          AACTGGCATCTCAGCACTCCGGCTTCAGTGGCTGGTCATATTCATGCTTGGTGTATTTGC
          CTTGGTCATTCCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
     10   AAATCCCTTCCTCCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
          GTAACTGTTCACTCAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
          AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTGTTCAATCCAATG
          ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAAACT
          TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).
```

AOLFR244 sequences:

```
          MWQEYYFLNVFFPLLKVCCLTINSHVVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
          MGLFNRKETSGLIFAIISIIFFTALMANGVMIFLIQTDLRLHTPMYFLLSHLSLIDMMYISTIVPKM
          LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSRRVCWMI
          IAGSWFGGSLDGFLLTPITMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVCCVLMLL
          IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSLFYGAAMYTYMLPHSYHKPAQ
          DKVLSVFYTILTIPMLNPLIYSLRNKDVTGALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).
```

```
          ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
     25   AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
          TACCTTATATCGGCACAACTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
          CACTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT
          ATCATCTTCTTCACCGCACTGATGGCCAATGGGGTTATGATCTTCCTGATCCAAACAGATT
          TGCGCCTTCATACACCCATGTACTTCCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT
     30   ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTAACCTGCTGGATCAAAGGACCATTTCCTT
          TGTGGGGTGCACAGCTCAACACTTCCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCCTG
          CTGGGGCTCATGGCCTATGACCGCTATGTGGCCATTGCAAACCCTCTGAGATACCCTGTCC
          TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTCCTGGTTTGGGGGCTCTTTGGA
          TGGCTTCCTCCTAACCCCCCATCACCATGAGCTTTCCCTTCTGCAATTCCCGGGAGATTAACC
     35   ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTCACGA
          GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCCTTTCTCTGTAGTCCTTGCTT
          CCTATGCCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
          CATTTGCCACTTGCTCATCCCACATGACTGTGGTGTCCTTGTTCTACGGGGCTGCCATGTAC
          ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCCAGGACAAAGTCCTCTCTGTGTTTT
     40   ACACCATTCTCACACCCATGCTGAACCCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
          TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCCTCAAAGGGTGTCAGGAGGTGT
          CTTTTGA (SEQ ID NO: 458).
```

AOLFR245 sequences:

```
     45   MDLKNGSLVTEFILLGFFGRWELQIFFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
          LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIMAFDRYVAICKP
          LHYRTIMSHKLLKGFAILSWIIGFLHESISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIBTYTLE
          LFVIADSGLLSFTCFILLLVSYIVILVSVPKKSSHGLSKALSTLSAHIIVVTLFFGPCIFIYVWPFSSL
          ASNKTLAVFYTVITPLLNPSIYTLRNKKMQEAIRKLRFQYVSSAQNF (SEQ ID NO: 459).
```

```
          ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
          GGGAACTTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
          AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCTTCATTCTCCCTTGTACTTTCT
          CCTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
     55   TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
          CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT
```

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
TTTGCGATACTTTCATGGATAATTGGTTTTTTACACTCCATAAGCCAGATAGTTTTAACAAT
GAACTTGCCTTTCTGTGGCCACAATGTCATAAACAACATATTTTGTGATCTTCCCCTTGTGA
TCAAGCTTGCTTGCATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTTTCTTACATTGTCATCCTGGTCAGTGTACC
AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCCACATCATTGTG
GTCACTCTGTTCTTGGACCTTGTATTTTATCTATGTTTGGCCATTCAGTAGTTTGGCAAG
CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLLGLPIRPEQQAVFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
HYTVIMREELCVFLVAVSWILSCASSLSHTLLLTRLSFCAANTIPHVFCDLAALLKLSCSDIFLNE
LVMFTVGVVVITLPFMCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLYYGSIFGQYLF
PTVSSSIDKDVIVALMYTVVTPMLNPFIYSLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
461).

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCTGTGTTCTTCACCCTGTTCCTGGGCATGTACCTGACACAGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCCATGTACTTCT
TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
TTTTTATAtTTTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGGATAT
GTTGCACATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC
AAGCTGTCCTGCTCAGATATCTTCCTCAATGAGCTGGTCATGTTCACAGTAGGGGTGGTGG
TCATTACCCTGCCATTCATGTGTATCCTGGTATCATATGGCTACATTGGGGGCCACCATCCTG
AGGGTCCCTTCAACCAAAGGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
TGGTGTCTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCCAGTGTGTAAGCAGTTCT
ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
CAACATTTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYLITVVGNLTMIILTKLDSHLHTPMYFSIRHL
ASVDLGNSTVICPKVLANFVVDRNTISYYACAAQLAFFLMFIISEFFILSAMAYDRYVAICNPLL
YYVIMSQRLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
LLSILFSVFNLISSFLIVLVSYMLLILLAICQMHSAEGRKKAFSTCGSHLTVVVVFYGSLLFMYMQ
PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACTCACAAGGCGGC
CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCCTCGTCATCTACCTAATCACAGTGGTGGGC
AACCTAACTATGATCATTTTGACCAAACTGGACTCCCACTTACATACACCTATGTACTTTTC
TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTTGTCCCAAGGTGCTGG
CAAATTTTGTTGTGGATCGAAATACTATTTCCTATTATGCATGTGCTGCACAGCTGGCATTC
TTCCTTATGTTCATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT
GGCCATTGTAACCCTCTGCTCTATTATGTTATTATGTCTCCAGCGACTGTGTCATGTACTGG
TGGGCATTCAATATCTCTACAGCACATTTCAGGCTCTGATGTTCACTATTAAGATTTTTACA
TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTTACTGTGATGATGTTCCTTTGCTACC
TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAAATT
TGATCTCCTCCTTTCTGATAGTCTTAGTGTCCTACATGTTGATTTTGTTAGCTATATGTCAA
ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTTGACAGTGG
TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5   **AOLFR248 sequences:**

MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIVVLSFYMVSILGNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSMVGSTLTMLLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFVVLPLGLILVSYGHIARAVLKIRSAEGR
10   RKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENCCGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA
15   CCCTCACTAGAAACTGTCCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACCTCCCCTTCCTGGACATGAGCTTCACCACGAGCATTGTCCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGGTCCAGTTCTAT
ATCTCCCATTGGCTGGGGGCAACCGAGTGTGTCCTGCTGGCCACCATGTCCTATGACCGCT
20   ACGCTGCCATCTGCAGGCCACTCCATTACACGTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTTGCGAGATGACCCCTCA
TTATGCAACTGGCTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGTCTTTGTTGTCCTGCCTCTGGGGCTCATCCTGGTCTCTTACGGGCCACATTGCCCGGGCCG
25   TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).
30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLLFWVLLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLLIYVTSLIGNIGMILLIKTDSRLQTPMYFFPQHLAFVDICYTSAITPKMLQSFTEEN
35   NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
NASVHTGFTFSLSFCKSNKINHFFCDGLPILALSCSNIDINIILDVVFVGFDLMFTELVIIFSYIYIM
VTILKMSSTAGRKKSFSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAATATAGAGCCATTTTATTGCAAAAAGTC
40   ACAAGGATGTTCCTGCTTTTCTGGGTCCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGGAAACAGCACTGAAGTGACTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTCAGCATGTCCTTTTCATTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC
CACAACATTTGGCTTTTGTTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45   AGCTTCACAGAAGAAAAATAATTTGATAACATTTCGGGGCTGTGTGGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATTCTTGC
50   CCTTTCATGCTCCAACATTGACATCAACATCCATTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCCTACATCTACATTATGGTCACCATCCTGAAG
ATGTCTTCTACTGCTGGGAGGAAAAATCCTTCTCCCACATGTGCCTCCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT
55   CTATAGCTTGAGAAATAAGGAAGGAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
STVMRPQVCALMLALCWVLTNIVALTHTFLMARLSFCVTGEIAHFFCDITPVLKLSCSDTHINE
MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVRTRGGVGKAFSTCSSHLCVVCVFYGTLFSAYLC
PPSIASEEKDIAAAAMYTIVTPMLNPFIYSLRNKDMKGALKRLFSHRSIVSS (SEQ ID NO: 469).

5

ATGGAAAACCAATCCAGCATTTCTGAATTTTTCCTCCGAGGAATATCAGCGCCTCCAGAGC
AACAGCAGTCCCTCTTCGGAATTTTCCTGTGTATGTATCTTGTCACCTTGACTGGGAACCTG
CTCATCATCCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCCATGTACTTTTTCTTGGC
CAACCTGTCTTTTGTTGACATGGGTTTAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
GATGTTTGGTGATCTAGACAGCTTCTTCCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
ATTTGCCACCCCCTCTGCTACTCCACAGTCATGAGGCCCCAAGTCTGTGCCCTAATGCTTGC
ATTGTGCTGGGTCCTCACCAATATCGTTGCCCTGACTCACACGTTCCTCATGGCTCGGTTGT
CCTTCTGTGTGACGTGGGGAAATTGCTCACTTTTTCTGTGACATCACTCCTGTCCTGAAGCTG
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
TCGTCCCCTTTTTATGCATTGTCACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCCACCTCTGCGTTGTTT
GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCCTCCCTCCATTGCCCTGCTAGAG
AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
TTGTTTCCTCTTAG (SEQ ID NO: 470).

10

15

20

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALEILLCGLFSAFYTLTLLGNGVIFGIICLDCKLHTPMYFFLSHLA
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVVMSYDRYADICHPLRY
NILMSWRVCTVLAVASWVFSFLLALVPLVLILRLPFCGPHEINHFCEILSVLKLACADTWLNQV
VIFAACVFILVGPLCLVLVSYLRILAAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVTYMAPK
SRHPEEQQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

25

30

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCATGTACTTCTTCC
TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAACTATGTCCCCAAGATGCTGACG
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
ATTTGGCTTTTGCTCACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCCTGG
CTGTGGCTTCCTGGGTGTTCAGCTTCCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG
CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCCTCAAGTT
GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTGCAGCCTGCGTGTTCATCCTG
GTGGGGCCACTCTGCCTCTGGTGCTGGTCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA
TCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCCACCTGCTCCTCCCACCTTTGCGTGGT
GGGACTCTTCTTTGGCAGCGCCATTGTCACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCCTGA
TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
AGGCTGACGTGA (SEQ ID NO: 472).

35

40

45

AOLFR252 sequences:

MRLANQTLGGDFFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
IDLTYISVTVPKMLVNQLAKDKTISVLGCGTQMYFYLQLGGAECCLLAAMAYDRYVAICHPLR
YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPFCRSHEIQHFFCEVPAVLKLSCSDTSLY
KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSSHIVVSLFYGAAIYNYML
PSSYQTPEKDMMSSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

50

55

-189-

```
   ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCCTGTTGGGAATCTTCAGCCAGA
   TCTCACACCCTGGCCGCCTCTGCTTGCTTATCTTCAGTATATTTTTGATGGCTGTGTCTTGG
   AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
   TATAAACCAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
5  GTGAACCAGCTGGCCAAAGACAAGAACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC
   TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
   ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
   CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
   TGAGCTTCCCCTTCTGCAGATCCATGAGATTCAGCACTTCTTCTGTGAGGTCCCTGCTGTT
10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
   CATGCTCCTGATACCTGTGACGGTCATTTCAGTGTCTTTACTACTATATCATCCTCACCATCC
   ATAAGATGAACTCAGTTGAGGGTCGGAAAAAGGCCTTCACCACCTGCTCCTCCCACATTAC
   AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACTACATGCTCCCCAGCTCCTACCAA
   ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAAATGCTGAGCGT
   GCAGAAACCTCCATATTAA (SEQ ID NO: 474).
```

AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL
ILLIHSEPRLHTPMYFFISQLALMDLMYLCVTVPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG
AEVFLLAAMAYDRYAAVCRPLHYPLLMNQRVCQLLVSACWVLGMVDGLLLTPITMSFPFCQS
RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRRKA
LATCSSHMIVLLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL
RSMMQSRMNQEK (SEQ ID NO: 475).

```
   ATGACTTTTTTTTTCCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
   CTCAGAATCAAACAGCAAGCACTGATTTCACCCTCACGGGACTCTTTGCTGAGAGCAAACA
   TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTTTCTTGATGGCCCTCACTGGGAATGCCC
   TCCTCATCCTCCTCACTCACGAGACCCCGCCTCCACACCCCCATGTACTTCTTTCATCAGC
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCAC
   AGGTCACTGGAGATGATACCATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
   GACCCTGGCTGGAGCTGAGGTTTTCCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
   GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
   CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTTGCTCACCCCCATTACCATGAGCTT
35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
   TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
   CTCACCCCCATCATGGTCATCTCCAGCTCATACACCCTCATCCTGCATCTCATCCACAGGAT
   GAATTCTGCCGCCGGCCGCAGGAAGGCCTTGGCCACCTGCTCCTCCCACATGATCATAGTG
   CTGCTGCTCTTCGGTGCTTCCTTCTACACCTACATGCTCCGGAGTTCCTACCACACAGCTGA
40 GCAGGACATGATGGTGTCTGCCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCCTCATTT
   ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
   ACCAAGAAAAGTAG (SEQ ID NO: 476).
```

AOLFR254 sequences:

MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
MDTLFICTTVPKLLADMVSKEKIISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
VLMNRKKCLLLAAGAWFGGSLDGFLLTPITMNVPYCGSRSINHFFCEIPAVLKLACADTSLYET
LMYICCVLMLLIPISIISTSYSLILLTIHRMPSAEGRKKAFTTCSSHLTVVSIFYGAAFYTYVLPQS
FHTPEQDKVVSAFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACCSSAQKVATSDA (SEQ ID NO:
477).

```
   ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
   CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT
   CATGATATTCTTGATTCAGGTGGACTCTCGCCTCCACACCCCCATGTACTTCTTGCTCAGTC
   AGCTGTCCATCATGGACACCCTTTTCATCTGTACCACTGTCCCAAAACTCCTGGCAGACAT
55 GGTTTCTAAAGAGAAGATCATTTCCTTTGTGGCCTGTGGCATCCAGATCTTCCTCTACCTG
```

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
CTGTAACCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCCTCATGTTG
CTCATCCCCATCTCTATCATCTCCACTTCCTACTGCTTGTTAACCATCCACCGCAT
GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTTCCTCCCACTTGACTGTAGTT
AGCATCTTCTATGGGGCTGCCTTCTACACATAACGTGCTGCCCCAGTCCTTCCACACCCCG
AGCAGGACAAAGTAGTGTCAGCCTTCTATACCATTGTCACGCCCATGCTTAATCCTCTCAT
CTACAGCCTCAGAAACAAGGACGTCATAGGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSRLHTPMYFLLSQLS
LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
YPVLMSRKICWLIVAAAWLGGSIDGFLLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY
ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQKVVGRCVSSGKVTTF (SEQ
ID NO: 479).

ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTTGACCTCCATAGCCAGC
AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCACCACCCCCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG
GTCGACCAGGTGATGAGCCAGAGAGCCATTTCCTTTGCTGGATGCACTGCCCAACACTTCC
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCCTCCTAGGACTCATGTCCTATGATCGCTAC
GTAGCCATCTGCAACCCTCTGCACTATCCTGTCCTCATGAGCCGCAAGATCTGCTGGTTGA
TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT
GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
TGAAGCTCTCCTGCACGGACACATCAGCCTCACGAGACAGCCATGTATGTCTGCTGTATTAT
GATGCTCCTCATCCCTTTCTCTGTCATCTCGGGCTCTTACAACAAGAATTCTCATTACTGTTT
ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCCACACATGG
TGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACAACCATCCTTACTCCCATGCTCAATC
CACTCATTTACAGCCTTAGGAACAAGGATGTCACAGGGGCCCTACAGAAGGTTGTGGGGA
GGTGTGTGTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGIICLDSKLHTPMYFFLSHL
AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFAVTECLILVVMSYDRYVAICHPF
QYTVIMSWRVCTILASTCWIISFLMALVHITHILRPPFCGPQKINHFICQIMSVFKLACAGPRLNQ
VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPVMGRAADRLTLPAPSHLCMVGLLFGSTMVM
YMAPKSRHPEEQQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
481).

ATGGGGAGGCAAGCAGCCCTGGGTCACAGAATTCATCCTGGTGGGGATTCCAGGTTGGTCCA
GCACTGGCGATTCTCCTCTGTGGGACTCTTCTCTGTCTTCTATACACTCACCCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCATGTACTTCTTCC
TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
TATTTGGCTTTTGCTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
GGCCATCTGCCACCCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTGCTCATATAACTCATATTCTGAG
GCCGCCTTTTGTGGCCCACAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
AATTGGCCTGTGCTGGCCCCTAGGCTCAACCAGGTGGTCCTATATGCGGGTTCTGCGTTCAT
CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACTTGCACATCCTGTCGCGCGCCATCTT

```
      GAGGATCCAGTAATGGGGAGGGCCGCAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT
      GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA
      CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
      CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG
  5   AAACAGAGATCAAAGTGA (SEQ ID NO: 482).
```

AOLFR257 sequences:

```
      MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLDSRLHTPMYVFLSHL
 10   AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFAITECLILVMMCYDRYVAICHPL
      QYTLIMNWRVCTVLASTCWIFSFLLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN
      QVVLFAGSAFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVMYM
      APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).
```

```
      ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
 15   GCTCTGGAGTTGTTCCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
      TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCTATGTATGTCTTC
      CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
      CAAATCTTGTGATGCACAAAAAAGTCATCTCCTTTGCTCCTTGCATACTTCAGACTTTTTTG
      TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
 20   TGGCAATCTGTCACCCCTTGCAATACACCCTCATTATGAACTGGAGAGTGTGCACTGTCCT
      GGCCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
      GGCTGCCTTTTTGTGGCCCACAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
      AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCCTATTTGCGGGTTCTGCGTTCA
      TCTTAGTGGGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
 25   AGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCTACCTGCTCCTCCCACCTCTGGG
      TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCCAAGTCAAGCCATTC
      TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
      CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTGCCTTTGGAAA
      CAGAGATCAATGTGA (SEQ ID NO: 484).
```

```
 30
```

AOLFR259 sequences:

```
      MGDNQSRVTEFILVGFQLSVEMEVLLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
      AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMSYDRFVAICHPL
 35   HYTVIMNWRVCTVLAITSWACGFSLALINLILLLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
      EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFSTCSSHLCVVGLYFGMAMVVY
      LVPDNSQRQKQQKILTLFYSLFNPLLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
      485).
```

```
      ATGGGGGACAACCAATCACGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
 40   GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
      TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCCATGTACTTCTTCC
      TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
      AAACCTAGTGAAACACAAAAAAACTATCTCGTTCATCTCTTGCATTATGCAGATGGCTTTG
      TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
 45   GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
      GCTATTACTTCCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTCAAG
      GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCATTCTTGTGGTGAAATTCTGTCTGTCCTC
      AAACCTGGCCTGTGCAGACACCTGGATTAATGAAATTTTTGTCTTTGCTGGTGGTGTGTTTG
      TCTTAGTCGGGCCCCTTTCCTTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCTGCCATCCTG
 50   AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCCACCTCTGTG
      TGGTTGGGCTTTACTTTGGCATGGCCATGGTTGTTTACCTGGTCCCAGACAACAACAGTCAACG
      ACAGAAGCAGCAGAAAATTCTCACCCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
      CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
      AAGAGGACCATGTGA (SEQ ID NO: 486).
```

```
 55
```

AOLFR24B sequences:

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTNKTISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
5   IIYGLMVISYIIVDVILIASSYVLILRAVFRLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCCTTCTTCCTCCTGCTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTTCTTTCCCATTCTGTATTGTGTACCTGATTGCCATTG
10   TGGGGAATATGACCATTCTCTTTGTGATCAAAACTGAACATAGTCTACACCAGCCCATGTT
CTACTTCCTGGCCATGTTGTCTATGATTGATCTGGGTCGTGTCCACATCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
GTTCTTTATTCACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCTGCAACCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
15   TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT
TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT
20   GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTCTTTTATGACACATCGTTTTGGCCAA
AACATTCCCCACTATATCCATATTCTTTGGCTAACCTGTATGTGGTTGTCCCACCTGCCCT
TAACCCTGTCATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
GTACAGAAAGAATAA (SEQ ID NO: 488)

25   **AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLEDVHVWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP
LRYSMILTNKVIAILGIVIIVRTLVFVTPFTFLTLRLPFCGVRIIPHTYCEHMGLAKLACASINVIY
GLIAFSVGYIDISVIGFSYVQILRAVFHLPAWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF
30   GHNIPHYIHILLANLYVVFPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCCTCGTAGTGGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
35   TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
TTTTACTTCCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
AGATGCTGGGAATTTTCTGGTTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
40   TAGCCATTCTGGGCATAGTCATCATTGTCAGGACTTTGGTATTTGTGACTCCATTCACATTT
CTCACCCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
GTGGGATGCATTGACATTTCTGTGATTGGATTTTCCTATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
45   GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCCTTCATGACACACCGCTTTGGCCACAA
CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTCCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA
ATAA (SEQ ID NO: 490)

50
AOLFR112B sequences:

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILILTLLDSHLQTPMYFFLRNFSF
LEISFTNIFIPRVLISITTGNKSISFAGCFTQYFFAMFLGATEFYLLAAMSYDRYVAICKPLHYTTI
MSSRICIQLIFCSWLGGLMAIIPTITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVVFL
55   VASVTLVVTLVLVILSYAFIIKTILKLPSAQQRTKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
DTFNKGVALLITSVAPLLNPFIYTLRNQQVKQPFKDMVKKLLNL (SEQ ID NO: 491)

-193-

```
     ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
     TCCAGGTGGCAGTTTTCACCTTTCTTTTCCTTGCGTATTTACTCAGCATCCTTGGAAATCTG
     ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
5    GAACTTCTCCTTCTTGGAAATTTCCTTCACAAACATCTTCATTCCAAGGGTCCTGATTAGCA
     TCACAACAGGGAACAAAGAGTATCAGCTTTGCTGAGTGCTTCACTCAGTATTTCTTTGCCAT
     GTTCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
     ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
     TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCCTGATGAGTCAGCA
10   GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
     CTCTCATGTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTTGGCATCGTGACCC
     TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCATTATCATAGGAACTATTCTGAAG
     CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTCCACATGTTCTTCCCACATGATTGTCAT
     CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
15   ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
     TTACACCCTAAGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCT
     GAATCTTTAA (SEQ ID NO: 492)


     AOLFR130B sequences:

20   MEGKNQTAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
     ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
     YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFHLPFCGNNQINYFFCDIPPLLILSCGDTSLNE
     LALLSIGILISWTPFLCHLSYLYIISTLRIRSSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISSYS
     LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25

     ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
     ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
     AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
30   CCTAGGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
     GTGCATCTTCCTGTCAGAGAAGAAAATCATTTCCTATAGGAGGCTGTGTGACCCAGCTCTTTG
     CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGGATAT
     ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT
     TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTCTGTGACCTT
35   CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
     TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC
     ATAAGCTGGACTCCTTTCCTGTGCATCACCTTCTTTCTTTACCTTTACATCATCTCCACCATCCT
     GAGGATCCGTTCCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCCACCTGCTC
     ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC
40   TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTCACACCCATGCTGAATCCT
     GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
     TGGCAGCCACCAGTTTTCTCTTCTGATATATAA (SEQ ID NO: 494)


     AOLFR142B sequences:

     MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFLSIYLFTVVGNLGLILLIRADTSLNTPM
45   YFFLSNLAFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
     VAICNPLLYMVVMTPGICIQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLLRL
     TCSDTRFKQLWIFACAGIMFISSLLIVFVSYMFIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
     TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:
     495)

50

     ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
     GCCTCACAGACCATCAGGAGTTGAAGATGCCCCTCTTTGTGCTATTCTTTATCCATCTACCTC
     TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
     CACCAATGTACTTCTTTCTTTCTTAGCAACCTAGCTTTTGTAGATTTCTGTTATTCTTCTGTCATT
55   ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
     CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG
```

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTCAC
ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT

5   GCCTGTGCTGGTATCATGTTCATTTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTCATC
ATTTCTGCCATCCTGAGGATGCATTCAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGCTTCTTCTACACAGTGATCATTC
CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA

10   AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL

15   AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMAYDCYVAICSPL
HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDDLPFLALSCSDTHMK
EILIFAFAGFDMISSSSIVLTSYIFIIAAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLQPKS
NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILTFLKIRKLY (SEQ
ID NO: 497)

20   ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCATTCTGAAAGGAATTACCAACCGGC
CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTTAGTTATCTATCTGGTCACAGTGCTGGG
CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG

25   GTGAATTTTGTTGTGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACTGGGTT
GTTTTCTCACCTTCATGATCACTGAGTGTTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT
GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
TGGTGGCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
CGTCTGACTTACTGTGGCCCAAACTTAATTAACCATTTCTATTGTGATGACCTCCCCTTCTT

30   AGCTCTGTCCTGCTCAGACACACACATGAAGGAAATTCTGATTGGCCTTTGCTGGCTTT
GATATGATCTCTTCCTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTCCACCTGTGGCTCCCATATGGTGA
CTGTCACTATTTTCTATGGCACACTGATCTTTGTTACTCCTACAGCCCAAATCAAATCACTCC
TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC

35   TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
GTTGTGAAAACTTACAGATATTAACATTTTTAAAAATAAGAAAACTTTATTAA (SEQ ID NO:
498)

AOLFR225B sequences:

40   MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTIITLTLLDPHLQTPMYFFLRNFSF
LEISFTSIFIPRFLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI
LLAVVTLMVTLVLVTLSYTYIIRTILRIPSAQQRTKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
GGAFNKGIAVLITSVTPLLNPFIYTLRNQQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45   ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
TCCAAGTGATGATATTCATCTTTCTGTTCCTCACCTACATGCTAAGTATCCTAGGAAATCTG
ACTATTATCACCCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCCTCCG
GAATTTCTCCTTCTTAGAAATTTCCTTCACATCCATTTTTATTCCCAGATTTCTGACCAGCA
TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTTGCTAT

50   ATTTCTTGGAGCTACCGAGTTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
TCTGCAAACCCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
CTGCTCCTGGTTGGGGGGATTCCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGGTGGAGCT
TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC

55   ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACACATCATTATCAGGACTATTCTGAGGA
TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCCTCCCACATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPELHILSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPHILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL
CVHLVVASVISGLFLSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVVCAQSHIHEQSVLVAAIL
10   AIAVPFFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCCTGGCCTATCCCTCCTGCCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTCAC
15   ACAGAAACCTGTCTATGCACATCCATGTACTATTTCCTGGGCAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGCCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGCTGAT
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
20   TGTTCCTGTCCTTACAACTGGTGGCCTTCATCTTCTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGCTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGTGCTGCTGCAGTATGGCTGCTGT
25   GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCCAGAACAGCTAG
(SEQ ID NO: 502)

30   **AOLFR276B sequences:**

MGGFGTNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIIKEEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFDHYVAICNP
LRYATVLTDVRVAHNGISIVIRSFCMVFPLPFLLKRLPFCKASVVLAHSYCLHADLIRLPWGDT
TINSMYGLFIVISAFGVDSLLILLSYVLIILHSVLAIASRGERLKTLNTCVSHIYAVLIFYVPMVSVS
35   MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTTTATGCTATTTCCTT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG
40   TACTACTTCCTGTCTCTTTTTCTGTTAATGACCTGGGTGTGTCCTTTTCTACATTGCCCCACT
GTACTGGCTGCTGTGTGTGTTTTCATGCCCCAGAGACAACTTTTGATGCCTGCCTGGCCCAGA
TGTTCTTCATCCACTTTTCCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCACAATGGCATATCCATTGTCATCCGCAGCTTCTGCATGGTGTTCCCACTTCCCTTCCTC
45   CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCCATTCCTACTGTCTGCATG
CAGACCTGATTCGGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTCAT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
ACATATCTATGCAGTGCTGATCTTCTATGTGCCCATGGTTAGTGTGTCCATGGTTCACCGAT
50   TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFFLLGITNNPEMKVTLFAVFLAVYIINFSANLGMIVLIRMDYQLHTPMYFFLS
55   HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDRYKAIINP
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPPLLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHSAEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5

ATGGACTGGGAAAATTGCTCCTCATTAACTGATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAGTGATGGCCTTTGATCGGTACA

10 AGGCCATCATCAACCCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTTATTCACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTCAGGAGTTTTCATTTCTTATTGTTATATCATCCTATCAGTCTTG

15 GAGATACACTCTGCTGAGGGGAGGTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG
CGGTTGCAATTTTCCAGGGAACTCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTGGTTCCCATGTTGAACCCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFVLFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG

25 NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIECFLFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCHSSILTSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA

30 GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
AAATGTGCTCATCCTTGTTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGTCCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC

35 ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCATTCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAATCACAATATCTATCTT

40 AAGCATTCGTACAACTGAGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA
MLDSIDLSLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL

50 WYTMILTSKIISLIAGIAVLRSLYMVIPLVFLLLRLPFCGHRIIPHTYCEHMGIARLACASIKVNIM
FGLGSISLLLLDVLLIILSHRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
DIPQYIHIFLANLYVVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCCATACTTCTTCATTCCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC

55 TGGGAAATGCTGCTATCTTCTTTGTGATCCAAACTGAACAGAGTCTCCATGAGCCCATGTA
CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCCAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
GCCTCATTGCAGGCATTGCTGCTGTCCTGAGGAGCTTGTACATGGTCATTCCACTGGTGTTTCT
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
5   GCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
TTCTCTCTTGTTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
GATATTCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCTCCCACCCT
10   CAATCCTGTAATCTATGGGGTCAGAACCAAACATATTAGGGAGACAGTGCTGAGGATTTTC
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

MALGNHSTITEFLLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLLVIRADSCLHKPMYFFLSH
15   LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFVTAGTEACLLSGMAYDRHAAIRRP
LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20   ATGGCCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCCTGGGGATTTACCTCCTGACCATAATGGA
AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
TCCTGAGTCACCTCTCTTTTGTTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG
25   GAGAACCTCCTGTCACAGAGGAAAACCATTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
TAAACATGGTCTTTTGTGAAGCCAAAATCATTCACCACTACAGCTATGAGATGCCATCCCT
30   CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCCACCTCA
CTGCAGTGACACTTTACTATGGCTCAGGTTTGCTCCGCCATCTCATGCCAAACTCAGGTTC
CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCCTCA
35   TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT
TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

CLAIMS

What is Claimed:

        1.   An isolated nucleic acid sequence selected from the group consisting of:

5   (i)   an isolated nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID

10   NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID

15   NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

20   NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

25   SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID

30   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID

NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,

SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID

5   NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,

SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID

NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,

10   SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,

SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,

SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

15   NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID

NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,

SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,

20   SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,

SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID

NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,

SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

25   NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID

NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,

SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512, or a fragment thereof

which comprises at least 75 nucleotides;

30   (ii)   an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a

polypeptide having an amino acid sequence selected from the group consisting of:

SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ

ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ

-200-

ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ

ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ

ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ

ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ

5   ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ

ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ

ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ

ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ

ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,

10   SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID

NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,

SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID

NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,

SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID

15   NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,

SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID

NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,

SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID

NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,

20   SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID

NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,

SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID

NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID

25   NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,

SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,

SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID

NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

30   SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID

NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,

SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID

NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,

SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID

NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,

SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID

NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,

SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID

NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,

SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID

NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,

SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID

NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,

SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID

NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,

SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID

NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,

SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID

NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,

SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID

NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,

SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID

NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,

SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, or a fragment thereof

which encodes at least 25 contiguous amino acids of said polypeptide;

. (iii)   a nucleic acid sequence that comprises at least 30% sequence identity with an

isolated nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2,

SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12,

SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22,

SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32,

SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42,

SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52,

SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62,

SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72,

SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82,

SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92,

-202-

SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID
NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

-203-

NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID

NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,

SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

5   NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,

SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,

SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID

NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,

10   SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID

NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,

SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or to a fragment thereof

15   which comprises at least 100 contiguous nucleotides thereof;

(iv)   a nucleic acid sequence that encodes a polypeptide having at least 40%

sequence identity at the amino acid level with a polypeptide having an amino acid

sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ

ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID

20   NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID

NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID

NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID

NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID

25   NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID

NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID

NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ

ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,

30   SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID

NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,

SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,

SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243; SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a nucleic acid sequence encoding at least 50 contiguous
amino acid residues thereof;

(v)   an isolated nucleic acid sequence which encodes an olfactory receptor or a
fragment thereof that specifically hybridizes and exhibits at least 30% sequence
identity under stringent conditions to a nucleic acid sequence selected from the group
consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID
NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID
NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID
NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID
NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID
NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID
NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID
NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID
NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID
NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID
NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108,
SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID
NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126,
SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID
NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144,
SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID
NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162,
SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID
NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180,
SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID
NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198,

-206-

SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234,

5   SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

10   NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,

15   SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID

20   NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,

25   SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID

30   NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID

-207-

NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,

SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512;

(vi)   an isolated nucleic acid sequence that specifically hybridizes to (i) or a portion

thereof under stringent hybridization conditions that is at least 20-30 nucleotides in

length; and

(vii)   a naturally occurring allelic or synthetic variant of a nucleic acid sequence

according to (i) or (ii), containing at least one substitution, deletion or addition

mutation in the coding region.

2.   The isolated nucleic acid sequence of Claim 1 which is selected from

the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID

NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID

NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID

NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID

NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID

NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID

NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID

NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID

NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID

NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID

NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106,

SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID

NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124,

SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID

NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142,

SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID

NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160,

SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID

NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178,

SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID

NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196,

SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID

NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214,

SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID
NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232,
SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID
NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250,
SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID
NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268,
SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID
NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286,
SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID
NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304,
SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID
NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322,
SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID
NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340,
SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID
NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358,
SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID
NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376,
SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID
NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394,
SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID
NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412,
SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID
NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430,
SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID
NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448,
SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID
NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466,
SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID
NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484,
SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID
NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502,
SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID

NO: 512 or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

3.   The isolated nucleic acid sequence of Claim 1 which encodes a
polypeptide having an amino acid sequence selected from the group consisting of:
SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ
ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ
ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ
ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ
ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ
ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ
ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ
ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ
ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,
SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID
NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,
SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID
NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,
SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID
NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,
SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID
NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,
SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID
NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,
SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID
NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,
SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID
NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,
SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID
NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,
SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

-210-

NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,
SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID
NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,
SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,
SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof
encoding at least 25 contiguous amino acid residues of said polypeptide.

4.   An isolated nucleic acid sequence having at least 30-60% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
5   NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
10   ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
15   SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
20   NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
25   SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
30   NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,

SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID

NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,

SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

5   NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,

SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,

SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

10   SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID

NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,

SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,

SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

15   NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,

SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID

NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,

SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

20   SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID

NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,

SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512; or a fragment thereof

comprising at least 100 contiguous nucleotides of any of said sequences.

25   5.   An isolated nucleic acid sequence having at least 60-80% sequence

identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID

NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID

30   NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID

NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID

NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID

NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID

NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,

SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID

NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,

SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID

NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,

SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID

NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ. ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID

NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,

SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID

NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,

SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID

NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,

SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID

NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,

SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,

SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
5   NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
10 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
15 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

6.   An isolated nucleic acid sequence having at least 80-90% sequence
20 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
25 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
30 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

-216-

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,

SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,

SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID

5   NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,

SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID

NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,

10   SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof

comprising at least 100 contiguous nucleotides of any of said sequences.

7.   An isolated nucleic acid sequence having at least 85% sequence

identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

15   NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID

NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID

NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID

NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

20   NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID

NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID

NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

25   ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID

NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

30   SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,

SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID

NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

-217-

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or a fragment thereof

5   comprising at least 100 contiguous nucleotides of any of said sequences.

8.   An isolated nucleic acid sequence having at least 90% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

10   NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

15   NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

20   SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

25   NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,

30   SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

-219-

SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

5   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

10   NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,

15   SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID

20   NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,

25   SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID

30   NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

9.   An isolated nucleic acid sequence according to Claim 1 which encodes
a polypeptide having at least 40-60% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
5   NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
10   NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
15   SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
20   NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
25   SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
30   NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID
NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

-221-

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,

SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID

NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,

SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID

5   NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,

SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID

NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,

10   SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,

SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID

NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,

SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID

15   NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID

NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,

SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID

NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,

20   SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,

SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID

NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,

SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID

25   NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,

SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least

40 contiguous amino acids thereof.

10.   An isolated nucleic acid sequence according to Claim 1 which encodes

30   a polypeptide having at least 60-70% sequence identity with a polypeptide having an

amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID

NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID

NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

-222-

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID

NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID

NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID

5   NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID

NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID

NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ

ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,

10   SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,

SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID

NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,

SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID

15   NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID

NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,

SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID

NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,

20   SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID

NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,

SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID

NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,

SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID

25   NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,

SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID

NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,

SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,

30   SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID

NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,

SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID

NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
5   SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
10   NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
15   SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
20   NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

11.   An isolated nucleic acid sequence according to Claim 1 which encodes
25   a polypeptide having at least 70-80% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
30   NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

-224-

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID

NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID

NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ

ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,

5   SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,

SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID

NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,

SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID

10   NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID

NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,

SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID

NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,

15   SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID

NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,

SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID

NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,

SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID

20   NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,

SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID

NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,

SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,

25   SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID

NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,

SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID

NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

30   NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,

SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID

NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,

SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,

SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID

NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,

SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID

5   NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID

NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,

SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID

NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,

10   SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,

SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID

NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,

SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID

15   NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,

SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least

40 contiguous amino acids thereof.

        12.   An isolated nucleic acid sequence according to Claim 1 which encodes

20   a polypeptide having at least 80-90% sequence identity with a polypeptide having an

amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID

NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID

NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

25   NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID

NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID

NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID

NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID

30   NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID

NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ

ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,

SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID
NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

13.   An isolated nucleic acid sequence according to Claim 1 which encodes
a polypeptide having about 90-99% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

-228-

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
5   SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
10   NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID
NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
15   SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
20   NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
25   SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
30   NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,

SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID

NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,

SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID

5   NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,

SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least

40 contiguous amino acids thereof.

14.   An isolated nucleic acid sequence which exhibits at least 50%

10   sequence identity with a nucleic acid sequence selected from the group consisting of:

SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ

ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ

ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ

ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ

15   ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ

ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ

ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ

ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ

ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ

20   ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100,

SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID

NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118,

SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID

NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136,

25   SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID

NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154,

SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID

NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172,

SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID

30   NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190,

SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID

NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208,

SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID

-230-

NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID
NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244,
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID
5   NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,
SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
10   SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID
15   NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
20   SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID
25   NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
30   SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid

sequence which exhibits at least 50% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence.

15.   An isolated nucleic acid sequence which exhibits at least 60% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,

SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID
NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID
NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid
sequence which exhibits at least 60% sequence identity to a fragment comprising at
least 100 contiguous nucleotides of said nucleic acid sequence.

16.   An isolated nucleic acid sequence that exhibits at least 70% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

-233-

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID

NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID

NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID

5   NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID

NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID

10   NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID

NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

15   NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,

SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID

NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

20   SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,

SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID

NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,

SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID

25   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID

NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,

SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

30   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID

NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,

SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID

NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
having at least 70% sequence identity with a fragment thereof comprising at least 100
contiguous nucleotides thereof.

17.   An isolated nucleic acid sequence that exhibits at least 80% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID

NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID

5   NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID

NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

10   NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,

SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID

NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

15   SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,

SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID

NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,

SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID

20   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID

NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,

SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

25   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID

NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,

SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID

NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

30   NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,

SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID

NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,

SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

-236-

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

5   NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,

10   SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

15   NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
having at least 80% sequence identity with a fragment thereof comprising at least 100

20   contiguous nucleotides thereof.

        18.   An isolated nucleic acid sequence that exhibits at least 85% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

25   NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

30   NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID

NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID

5   NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,

SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID

NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

10   SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,

SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID

NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,

SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID

15   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID

NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,

SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,

20   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID

NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,

SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID

NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

25   NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,

SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID

NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,

SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,

30   SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,

SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
having at least 85% sequence identity with a fragment thereof comprising at least 100
contiguous nucleotides thereof.

19.   An isolated nucleic acid sequence that exhibits at least 90% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
5   SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
10   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
15   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
20   NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
25   SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
30   NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

5 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 90% sequence identity with a fragment thereof comprising at least 100

10 contiguous nucleotides thereof.

20. An isolated nucleic acid sequence that exhibits at least 95% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

15 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID

20 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,

25 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID

30 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
5   NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
10   SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
15   NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
20   SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
25   NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
30   SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
having at least 95% sequence identity with a fragment thereof comprising at least 100
5   contiguous nucleotides thereof.

21.   An isolated nucleic acid sequence that exhibits about 96-99% sequence
identity with a nucleic acid sequence encoding an olfactory receptor selected from the
group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8,
10   SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18,
SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28,
SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38,
SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48,
SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58,
15   SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68,
SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78,
SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88,
SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98,
SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID
20   NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116,
SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID
NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134,
SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID
NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152,
25   SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID
NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170,
SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID
NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188,
SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID
30   NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206,
SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID
NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224,
SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID

-243-

NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242,
SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID
NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260,
SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID
NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278,
SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID
NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296,
SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID
NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314,
SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID
NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332,
SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID
NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350,
SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID
NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368,
SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID
NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386,
SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID
NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404,
SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID
NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422,
SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID
NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440,
SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID
NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458,
SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID
NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476,
SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID
NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494,
SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID
NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512
or a fragment having at least 96-99% sequence identity with a fragment thereof
comprising at least 100 contiguous nucleotides thereof.

-244-

22.   A nucleic acid sequence which encodes for a functional olfactory receptor polypeptide, wherein said nucleic acid sequence comprises a portion which is at least 100 nucleotides in length and exhibits at least 40% sequence identity with at

5   least 100 contiguous nucleotides of a portion of an olfactory receptor encoding a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID

10   NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID

15   NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130,

20   SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID

25   NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220,

30   SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256,

SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID
NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274,
SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID
NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292,
SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID
NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310,
SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID
NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328,
SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID
NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346,
SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID
NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364,
SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID
NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382,
SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID
NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400,
SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID
NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418,
SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID
NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436,
SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID
NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454,
SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID
NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472,
SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID
NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490,
SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID
NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508,
SEQ ID NO: 510 and SEQ ID NO: 512.

23.   The nucleic acid sequence of Claim 22 which is a chimeric nucleic acid
sequence, wherein said nucleic acid sequence is produced by combining portions of at
least two different G protein-coupled receptors.

-246-

24.   The chimeric nucleic acid sequence of Claim 23 wherein said two different G protein-coupled receptors are olfactory receptors.

5   25.   The chimeric nucleic acid sequence of Claim 23 wherein said chimeric sequence contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said olfactory receptor encoding nucleic acid sequences.

26.   An isolated nucleic acid sequence according to Claim 1, wherein said
10   isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

27.   The nucleic acid sequence of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

15

28.   An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 40% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
20   NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
25   NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
30   NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

5　　NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

10　　SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

15　　NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

20　　SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID

25　　NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,

30　　SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,

-248-

SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
5   SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
is directly or indirectly attached to a sequence that facilitates the expression and/or
10   translocation of said polypeptide on the surface of a cell.

29.   An isolated nucleic acid sequence which encodes a polypeptide that
exhibits at least 50% sequence identity with a polypeptide selected from the group
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
15   NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
20   NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
25   SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
30   NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

-249-

NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,

SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID

NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

5   NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID

NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,

SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,

10   SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,

SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID

15   NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID

NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,

SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID

NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,

20   SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID

NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,

SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID

NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID

25   NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,

SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID

NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,

SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID

NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,

30   SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID

NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,

SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID

NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

30.   An isolated nucleic acid sequence which encodes a polypeptide that
exhibits at least 60% sequence identity with a polypeptide selected from the group
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

-251-

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID

NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,

SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

5   NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,

SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,

10   SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID

NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID

NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,

SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID

15   NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,

SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID

NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,

SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID

NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

20   SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID

NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,

SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID

NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,

SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID

25   NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,

SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID

NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,

SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID

NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

30   SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID

NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,

SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a

fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

5   31.   An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 70% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID

10   NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID

15   NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID

20   NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,

25   SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

30   NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

-253-

NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

5   NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,

10   SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID

15   NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,

20   SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID

25   NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

30   is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

-254-

32.   An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
5   SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
10   NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
15   SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
20   NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
25   SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

30   33.   An isolated nucleic acid sequence which encodes a polypeptide that
exhibits at least 85% sequence identity with a polypeptide selected from the group
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

-256-

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID

NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID

NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID

NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

5   NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID

NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID

NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID

NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,

10   SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID

NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,

SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID

NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,

SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

15   NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,

SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID

NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,

SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,

20   SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID

NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID

25   NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,

SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,

SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

30   SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,

SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID

NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

34.   An isolated nucleic acid sequence which encodes a polypeptide that
exhibits at least 90% sequence identity with a polypeptide selected from the group
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID

NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID

NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID

NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

5   NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,

SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID

NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,

SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID

NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,

10   SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,

SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID

NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,

SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

15   NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,

SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID

NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,

20   SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID

NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,

SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,

SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID

25   NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID

NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,

SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID

NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

30   SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID

NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,

SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID

NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,

SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

35.   An isolated nucleic acid sequence which encodes a polypeptide that
exhibits about 90-99% sequence identity with a polypeptide selected from the group
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
5   NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO:.151, SEQ ID
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
10 SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
15 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,
20 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
25 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
30 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

36. The isolated nucleic acid sequence according to Claim 26, wherein said isolated nucleic acid sequence is operably linked to a constitutive promoter.

37. The isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is operably linked to a regulatable promoter.

38. The isolated nucleic acid sequence of Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence encoding a mammalian rhodopsin polypeptide or a fragment thereof.

39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

-262-

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID

NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID

NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID

NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

5   NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID

NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID

NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ

ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,

SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

10   NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,

SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID

NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,

SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID

NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

15   SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID

NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,

SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID

NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,

SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID

20   NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,

SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID

NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,

SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID

NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,

25   SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID

NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,

SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,

SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID

30   NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,

SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID

NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
5 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
15 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
20 SEQ ID NO: 509, and SEQ ID NO: 511.

40.   The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 100 amino acids.

25   41.   The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 150 amino acids.

42.   The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 200 amino acids.
30

43.   The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 250 amino acids.

44.   The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is an olfactory G protein-coupled receptor.

45.   The isolated nucleic acid molecule of Claim 39, wherein the expression product binds an odorant.

46.   The isolated nucleic acid molecule of Claim 1 comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240,

SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID

NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258,

SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID

NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276,

5   SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID

NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294,

SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID

NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312,

SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID

10   NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330,

SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID

NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348,

SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID

NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366,

15   SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID

NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384,

SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID

NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402,

SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID

20   NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420,

SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID

NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438,

SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID

NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456,

25   SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID

NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474,

SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID

NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492,

SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID

30   NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510

and SEQ ID NO: 512.

47.   An expression vector that comprises a nucleic acid sequence according to Claim 1.

48.   The expression vector of Claim 47, wherein said vector is a mammalian, yeast, bacterial or insect expression vector.

49.   A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

50.   A mammalian cell according to Claim 49.

51.   A human cell according to Claim 50.

52.   A yeast or insect cell according to Claim 49.

53.   The mammalian cell according to Claim 49 which is selected from the group consisting of: an olfactory cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

54.   A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

55.   A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1, wherein the solid phase is attached to an array comprising at least one additional nucleic acid sequence.

56.   The solid phase according to Claim 55 which comprises an array of at least 4 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

57.   The solid phase according to Claim 55 which comprises at least 10 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

-267-

58.　　The solid phase according to Claim 55 which comprises at least 50 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

59.　　The solid phase according to Claim 55 which comprises at least 100 different sequences that encode olfactory receptors or fragments or variants thereof.

60.　　An isolated polypeptide that is selected from the group consisting of:

(i)　　a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

-268-

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

-269-

(ii)   a polypeptide comprising an amino acid sequence that exhibits at least 40%

sequence identity with an amino acid sequence selected from the group consisting of:

SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ

ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ

ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ

ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ

ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ

ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ

ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ

ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ

ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ

ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ

ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,

SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID

NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,

SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID

NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,

SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID

NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,

SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID

NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,

SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID

NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,

SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID

NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,

SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID

NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID

NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,

SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,

SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID

NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
5   .   SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,
SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
10   NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
15   SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
20   NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
25   SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

(iii)   a polypeptide comprising an amino acid sequence that exhibits at least 60%
sequence identity with a fragment of a polypeptide according to (i) which fragment is
at least 40 amino acids in length;

(iv)   a chimeric polypeptide that comprises a portion of a polypeptide according to
30   (i) or (ii) that is at least 40 amino acids in length and a portion of at least one other G
protein-coupled receptor; and

(v)   a variant of a polypeptide according to (i) which differs by said polypeptide by
at least one substitution, addition or deletion modification.

-271-

61.   An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 70% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

62.   An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits at least 80% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID

NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID

NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID

NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID

5   NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID

NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID

NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ

ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,

10   SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID

NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,

SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,

SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID

15   NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,

SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID

NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,

SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,

20   SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID

NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,

SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID

NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,

SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

25   NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,

SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID

NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID

NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,

30   SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID

NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,

SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID

NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID

NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,

SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID

NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,

5   SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID

NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID

NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,

SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID

10   NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,

SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID

NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,

15   SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID

NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,

SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID

NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,

SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID

20   NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509

and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

63.   An isolated polypeptide according to Claim 60 wherein said

polypeptide exhibits at least 90% sequence identity with a polypeptide having a

25   sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ

ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID

NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID

NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID

30   NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID

NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID

NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID

NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID

5   NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,

10 SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID

15 NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,

20 SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID

25 NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,

30 SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

64.   An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits about 80-90% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

-277-

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
5   NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
10   SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID
15   NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
20   SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
25   NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
30   SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

65.   An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits at least 90-95% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,

SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID

NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,

SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID

5 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,

SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,

SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID

NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

10 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID

NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,

SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID

NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,

SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID

15 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID

NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,

SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID

NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,

20 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID

NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID

NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,

SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID

25 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,

SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID

NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,

30 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID

NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,

SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID

NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,

SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

66.   An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 95-99% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

-281-

NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

67.   A variant according to Claim 60(v) which comprises at least 5
conservative amino acid substitutions.

-282-

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

5   69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

10

71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

72. A solid phase comprising at least one directly or indirectly

15   immobilized isolated polypeptide according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

73. The solid phase of Claim 72 comprising at least 4 different immobilized polypeptides according to Claim 60, or a cell which expresses said

20   polypeptide on the surface thereof.

74. The solid phase of Claim 72 comprising at least 16 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

25

75. The solid phase of Claim 72 comprising at least 25 different immobilized polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

30   76. A method of detecting expression of an olfactory receptor gene comprising (a) hybridizing at least one sample with a nucleic acid according to Claim 1 and (b) detecting expression of the olfactory receptor gene by a positive hybridization signal.

77.   A method of screening a library comprising (a) hybridizing the library with a nucleic acid according to Claim 1 and (b) detecting one or more olfactory receptor clones in the library by a positive hybridization signal.

78.   A recombinant polynucleotide comprising a nucleic acid according to Claim 1 attached directly or indirectly to a heterologous nucleic acid.

79.   An expression vector comprising the nucleic acid of Claim 1 and an operably linked heterologous nucleic acid that drives expression thereof.

80.   A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

81.   A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

82.   A method of making a recombinant polynucleotide comprising ligating the nucleic acid of Claim 1 to a heterologous nucleic acid.

83.   The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

84.   A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 79 into a host cell, and propagating the host cell in which the recombinant polynucleotide has been introduced.

85.   A method of detecting specific binding of a putative ligand to an olfactory receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the olfactory receptor is expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the olfactory receptor.

86.   A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-human organism, or propagating the host non-human organism in which the
5   recombinant polynucleotide has been introduced.

87.   An isolated protein molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID
10   NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
15   NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ
20   ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,
25   .SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID
30   NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID

NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241,

SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID

NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,

SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID

5   NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,

SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID

NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295,

SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID

NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313,

10   SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID

NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331,

SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID

NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349,

SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID

15   NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367,

SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID

NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385,

SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID

NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403,

20   SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID

NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421,

SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID

NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439,

SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID

25   NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457,

SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID

NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475,

SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID

NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493,

30   SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID

NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:

511.

88.   The isolated protein molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

89.   The isolated protein molecule of Claim 87, wherein the fragment contains at least 150 amino acids.

90.   The isolated protein molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

91.   The isolated protein molecule of Claim 87, wherein the fragment contains at least 250 amino acids.

92.   The isolated protein molecule of Claim 87, which is a functional olfactory receptor polypeptide.

93.   The isolated protein molecule of Claim 87, wherein the fragment specifically binds an odorant molecule.

94.   A recombinant polypeptide comprising the protein molecule of Claim 87 and a heterologous peptide domain.

95.   The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a G protein-coupled receptor transmembrane domain.

96.   The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with an olfactory receptor ligand-binding domain, wherein the olfactory receptor ligand-binding domain is a chimera of at least two different olfactory receptors.

97.   A method of detecting specific binding of a ligand to an olfactory receptor comprising (a) contacting the ligand with the protein of Claim 86, and (b) directly or indirectly detecting specific binding between the ligand and the olfactory receptor.

98.   An antibody or antibody fragment that specifically binds a polypeptide
having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1,
SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ
5   ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ
ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ
ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ
ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ
ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ
10   ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ
ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ
ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ
ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101,
SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID
15   NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119,
SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID
NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137,
SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID
NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155,
20   SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID
NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173,
SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID
NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191,
SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID
25   NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209,
SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID
NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227,
SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID
NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245,
30   SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID
NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263,
SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID
NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281,

-288-

SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID
NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299,
SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID
NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317,
SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID
NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335,
SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID
NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353,
SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID
NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371,
SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID
NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389,
SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID
NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407,
SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID
NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425,
SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID
NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443,
SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID
NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461,
SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID
NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479,
SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID
NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497,
SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID
NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

99.   A method of detecting specific binding of the antibody of Claim 98 to
an olfactory receptor comprising (a) contacting the antibody with a sample comprising
the olfactory receptor and (b) detecting specific binding therebetween.

100.   The method of Claim 99, wherein specific binding of the antibody to a
cell in the sample identifies the cell as an olfactory cell.

-289-

101.   A method of screening a library of chemical compounds for compounds that are involved in olfactory sensation comprising contacting compounds in said library with at least one polypeptide according to Claim 87 and identifying compounds that specifically bind to at least one of said polypeptides.

102.   The method of Claim 101 wherein said library is a combinatorial chemical library.

103.   The method of Claim 101 wherein said library is a peptide library.

104.   The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal peptidominetic, or small molecule organic compound library.

105.   The method of Claim 101 wherein said library is a random combination of compounds.

106.   The method of Claim 101 wherein said compounds are screened by high turning point screening.

107.   The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.

108.   A cell-based assay for identifying molecules that interact with an olfactory receptor comprising:
   obtaining a cell that expresses at least one polypeptide according to Claim 60 or a chimeric protein comprising a portion of said protein and that of another G protein-coupled receptor, and which optionally expresses at least one functional G protein;
   contacting said cell with a molecule to be screened for its ability to modulate an olfactory receptor; and
   detecting whether modulation occurs.

-290-

109.   The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.

110.   The method of Claim 108 wherein modulation is detected by measuring the transfer of 32P from gamma-labeled GTP to the olfactory receptor polypeptide.

111.   The method of Claim 108 wherein modulation is determined based on a comparison to a control compound known to modulate the particular olfactory receptor protein.

112.   The method of Claim 108 wherein the G protein is Gα15 or Gα16 or another promiscuous G protein.

113.   The method of Claim 108 wherein modulation is determined by detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114.   The method of Claim 108 wherein modulation is determined based on the level of transcription of said olfactory polypeptide after contacting the cell with the screened compound.

115.   The method of Claim 108 when said screened compounds are synthesized by computer assisted drug devices based on the predicted or actual three-dimensional structure of the amino acid sequence of the olfactory protein or a fragment thereof.

116.   The method of Claim 108 wherein compounds that modulate olfactory receptor are identified based on whether they specifically bind to a olfactory receptor polypeptide.

117.   The method of Claim 108 wherein modulation refers to the inhibition of olfactory receptor function.

118. The method of Claim 108 wherein modulation refers to the enhancement of olfactory receptor function.

119. A method for representing the olfactory perception of one or more odors in one or more mammals, comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammals; and

generating from said values a quantitative representation of odor perception, wherein at least one of said odor receptors is an odor receptor polypeptide having a sequence that is at least about 40% identical to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID

-292-

NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225,
SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID
NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243,
SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID
NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261,
SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID
NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279,
SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID
NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297,
SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID
NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315,
SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID
NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333,
SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID
NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351,
SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID
NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369,
SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID
NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387,
SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID
NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405,
SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID
NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423,
SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID
NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441,
SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID
NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459,
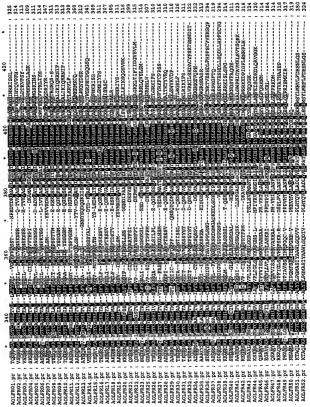SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID
NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477,
SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID
NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495,
SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID
NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

120.   The method of claim 119, wherein said representation constitutes a point or a volume in n-dimensional space.

5   121.   The method of claim 119, wherein said representation constitutes a graph or a spectrum.

122.   The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

10

123.   The method of claim 119, wherein said providing step comprises contacting a plurality of recombinantly produced olfactory receptors with a test composition, and quantitatively measuring the interaction of said composition with said receptors.

15

124.   A method for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of
20   molecules yielding known odor perception in a mammal,

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal;

providing values X_1 to X_n representative of the quantitative stimulation of each of n
25   odor receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown odor perception in a mammal;

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding unknown odor perception in a mammal; and

30   predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor perception in a mammal by comparing the quantitative representation of odor perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor

-294-

perception in a mammal to the quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal, wherein at least one of said odor receptors is a odor receptor polypeptide having a sequence that is at least about 40% identical to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO:243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO:, 263, SEQ ID NO:, 265, SEQ ID NO:

267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ

ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285,

SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID

NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303,

5   SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID

NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321,

SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID

NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339,

SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID

10   NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357,

SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID

NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375,

SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID

NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393,

15   SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID

NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411,

SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID

NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429,

SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID

20   NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447,

SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID

NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465,

SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID

NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483,

25   SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID

NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501,

SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID

NO: 511.

Figure 1

Figure 1

Figure 1

Figure 1

```
                                    440
               AOLFR01.pr :  ------------ :    ~
               AOLFR02.pr :  ------------ :    ~
               AOLFR03.pr :  ------------ :    ~
               AOLFR04.pr :  ------------ :    ~
               AOLFR05.pr :  ------------ :    ~
               AOLFR06.pr :  ------------ :    ~
               AOLFR07.pr :  ------------ :    ~
               AOLFR08.pr :  ------------ :    ~
               AOLFR09.pr :  ------------ :    ~
               AOLFR10.pr :  ------------ :    ~
               AOLFR11.pr :  ------------ :    ~
               AOLFR12.pr :  ------------ :    ~
               AOLFR13.pr :  ------------ :    ~
               AOLFR14.pr :  ------------ :    ~
               AOLFR15.pr :  ------------ :    ~
               AOLFR16.pr :  ------------ :    ~
               AOLFR17.pr :  ------------ :    ~
               AOLFR18.pr :  ------------ :    ~
               AOLFR19.pr :  ------------ :    ~
               AOLFR20.pr :  ------------ :    ~
               AOLFR21.pr :  ------------ :    ~
               AOLFR22.pr :  ------------ :    ~
               AOLFR23.pr :  ------------ :    ~
               AOLFR25.pr :  ------------ :    ~
               AOLFR26.pr :  ------------ :    ~
               AOLFR27.pr :  ------------ :    ~
               AOLFR28.pr :  ------------ :    ~
               AOLFR29.pr :  ------------ :    ~
               AOLFR30.pr :  ------------ :    ~
               AOLFR31.pr :  ------------ :    ~
               AOLFR32.pr :  ------------ :    ~
               AOLFR34.pr :  ------------ :    ~
               AOLFR35.pr :  ------------ :    ~
               AOLFR36.pr :  HSIPTSABPAP :  305
               AOLFR37.pr :  ------------ :    ~
               AOLFR38.pr :  EKGQPH----- :  300
               AOLFR39.pr :  ------------ :    ~
               AOLFR40.pr :  ------------ :    ~
               AOLFR41.pr :  ------------ :    ~
               AOLFR42.pr :  ------------ :    ~
               AOLFR43.pr :  ------------ :    ~
               AOLFR44.pr :  ------------ :    ~
               AOLFR45.pr :  ------------ :    ~
               AOLFR46.pr :  ------------ :    ~
               AOLFR47.pr :  ------------ :    ~
               AOLFR48.pr :  ------------ :    ~
               AOLFR49.pr :  ------------ :    ~
               AOLFR50.pr :  ------------ :    ~
               AOLFR51.pr :  ------------ :    ~
               AOLFR52.pr :  ------------ :    ~
```

Figure 1

Figure 2

Figure 2

Figure 2

Figure 2

Figure 3

Figure 3

Figure 3

Figure 3

Figure 4

Figure 4

Figure 5
2/5

3/4

Figure 4

Figure 4

Figure 5

Figure 5

Figure 5

Figure 5

5/5